STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To: Subject: Wednesday, December 03, 2003 1:57 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/674237

RECEIVED

PI ase rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Wednesday, December 03, 2003 1:54 PM

To:

Chan, Christina

Rush search request for 09/674237 Subject:

Please search in commercial database, issued patent files, PGPUB and interference:

SEQ ID NO:1, 2, and 3

Thank you.
MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Searcher:	
Phone:	_
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TYPE OF SEARCH:
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Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

/ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback Form
▶ I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
☐ Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention
Comments:

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Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

TITLE	AUTHORS	DESERVE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AF132478	RESULT 1
The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Eps15	Sengar,A.S., Wang,W., Bishav,J., Cohen.S. and Egan.S.E.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus	Mus musculus (house mouse)		AF132478.1 GI:4378884	AF132478	Mus musculus Esel protein mRNA, complete cds.	AF132478 3723 bp mRNA linear ROD 09-MAR-1999		

BASE COUNT ORIGIN Query Ma Guery Ma Best Loc Matches Qy Db Db Qy Db Qy Db Qy Db Qy Db	CDS	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICE
// Color 100 1	/organism="Mus musculus" /mol_type="mRNA" /db xref="taxon:10090" 1. 3642	EMBO J. 18 (5), 1159-1171 (1999) 99164083 10064583 2 (bases 1 to 3723) Sengar,A.S., Wang,W., Cohen,S., Bishay,J. and Egan,S.E. Direct Submission Direct Gubmission Submitted (02-MAR-1999) Programs in Cancer & Blood Research/Developmental Biology, The Hospital for Sick Children, 555 University Avenue, Toronto, ON MSG-1X8, Canada Location/Qualifiers 1. 3723
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AGTGTGGAGCTGGAGAAGCGCCCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCAGGAG
                                                                                               CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT
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                                                                    AGCTCTTCTGTGGATCAGAGGCTGCCTGAGGGAGCCGTCGTCAGAGGATGAGCAGCAG
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B1 AAAACAGGAGTTIAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCT B1 AAAACAGGGAGTTTAGGAAAAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCT	8 8	2101 GACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCA 2160	υ ≺
21 GAGTICTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGCTCTGGAACTGCTGGG 21 HILLIH	P &	2041 AAGAGGGAAGACTGTCAGGAAGAAGGAGGCGGAAGAGAGAG	5 ~
61 GTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGGACGGGAACGGTCGGT	b b	1981 GAGCATGTGCAGCAGGAGGAGGAGCAGCCCCCGGGAAACCCCCACGAGGAG	5 ~
001 ATTGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCACCAAGGGGAT 	dg Vy	1921 TTAGAGAAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTG 1980 	U ~
941 GCTAGTCTAAAGAGTGGCTTCCCCGGCCGCCAAGCCAGCC	dg Vo	19 19	· ~
2881 CTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCT 2940	D Qy	1801 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAG 1860 	٠ ٦
21 21	Db Qy	1741 CTCCGGGAGCAGCTGGACGAGGAGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGAT 1800 	J ~
61 AAAGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAGAC 2 	D QY	1681 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAG 1740 	5 7
701 GGCCAGGGTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTGGAGAGCCAAA	D 64	1621 ATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCAT 1680 	J ~
641 CGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCCCCATCTCCCGTCCTG	ע פ	1561 GCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTTGGAAGACTT 1620	J ~
581 GACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTACTGCTGGCCAGTTA	Db Qy	1501 CGACTGGCAACCCAGAGGCAAGAAATTGAGAGACCAAGAACTAAGAGAGCTAAGAAATT 1560 	U ~
S21 AACAACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAACGAAAGCCAGAAACG	dg dg	1441 TTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGT 1500 	J ~
61 GCTCTGCGTGARACCCCTGCTCCTTTGCCAGTGACCTCTTCTGAGCCCTCCACAACCCCC 61 GCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTCTGAGCCCTCCACAACCCCC	D QY	1381 AACAAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAGACTCTGGAGTTTGAG 1440 	5 ~
01 GAGGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCCTGCCCCCAAACTG	Db Qy	1321 GAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAGAGG 1380 	J ~
41	Db QY	1261 CAGCGAGAGGAGGAGGAGGAGGAGGAGGATCGAGAGGGCGGAGAGGCCGCAAAACGGGAACTG 1320 	0 ~
B1 CCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGGATGGCTTGGAGGA [B 5	1201 GAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAGCAGCGGGAGCTGGAGCCGG 1260	J ~
21	Db	41 CGGTTGGCTCAGCTGGAGCGCCGAGCAGGAGAGGAAAGAGCGGGAGCGCCAGGAGCAG 120	0 ~
	_	1081 AGTGTGGAGCTGGAGAAGCGCCGGCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCAGCAGCAG	U

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J. Biol. Chem. 274 (26), 18446-18454 (1999) 99303609
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Direct Submission
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Sciurognathi; Muridae; Murinae;
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YYRALYPESRSHIDE IT IQFOLI VMVKGEWUDESQTGEBFRUGGEFKOKTGWFPANY
EKI PENEI PTPAKPVTDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADPSSTWPS
STNEKEPSTDNNDTWAAQPSLTVVBSAGOLRQRSAFTPATATGSSEPSPVLGQGEKVEGL
AQALYPWRAKKUNHLINENKSDVITVLEQODMWHGESVOGKOWFPKSVKTLSGOPKK
STSIDTGFTEAPSSLKRVASPAAKPAI FGEEFVAMYTYESSEHGDLTFQQGHVIVVTK
KODMWTGTVGETSGVEPSNVVRLKDSEGSGTAGKTOSLEKKEIAQVIASTTATGPE
QLTLAPGQLILI RKANPGGWMEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELP
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3407; 661 641 601 581 541 521 481 461 421 401 361 341 281 181 161 121 101 781 761 721 701 301 241 221 61 41 щ Similarity GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGGATAGCGGGATTTATTACT ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA 660 AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG GGGGCCCCTCCTGTCATACAGCCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCCA GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA GGAATGTCTCCGCCCTTAGTATCTTCTGTCCCTCAAGCAGCAGTGCCTCCCCCTGGCTAAC GGAATGTCTCCACCCTTAGTATCTTCTGTCCCCTCCAGCAGCAGCGCCTCCCCCTGGCTAAC GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT GTCATGAAGCAGCCAGCGAGCGATCTCTAGTGCACCAGCGTTTGGTATAGGAGGGATG GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT GGTGATCAAGCAAGGAACTTCTTTTTCCAATCTGGGTTACCTCAGCCCGTCTTAGCACAA GAAAGAGCCAAGCATGACCAGCAGTTCCAGAGTTTGAAGCCGATATCTGGATTCATCACT ATGGCTCAGTTTCCCGACACCTTTTGGTGGGAGCCTGGACATCTGGGCCATAACCGTGGAG TCAATCTGGAATCTTTCCGACATTGATCAAGATGGAAAGCTCACCGCAGAAGAATTCATC ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT GCACAATCATI **AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAACTACAGAAG** GCTGGAATGCCACCACTGACAGCTGTTGCTCCCGTGCCAATGGGCTCCATCCCAGTTGTT Conservative .88.7**%**; 93.2**%**; Score 3229.8; Pred. No. 0; 0; Mismatches 0 232; Indels 18; Gaps 360 100 880 840 820 780 600 520 300 160 120 760 720 700 640 580 540 460 400 340 280 220 60

926 978 986
2858 CTGGAACAGCAAGACTCATTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC 2918 AAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC 2918 AAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC 2918 AAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC
6 8 6
2678 AGTGCTGGCCAGTTAAGGCAGAGGTCGCCACCAGCCACAGCCACTGGCTCCTCC 2686 CCATCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTAT
2566 RAMANCICAGAAACIGACKATACIGIGATACGIIGGGGCICAGCCTTCCTCACCGTACCGIACCGI
58
2446 CCTGCCCCAAACTGGCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTCTGAG
2386 AAGATTCCAGAAAATGAGGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCC
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1981 GAGCATGTGCAGCAGGAGGAGCAGCCACGCCCCCGGAAACCCCACGAGGAG
1921 TTAGAGAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTG

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                                                                                                                                       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5381)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant

Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M.

Alu-splice cloning of human Intersectin (ITSN), a putative

multivalent binding protein expressed in proliferating and

differentiating neurons and overexpressed in Down syndrome

Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                                                                                                                                                                                                                                          5381 bp mRNA
Homo sapiens intersectin short isoform
AF114488
AF114488.1 GI:4808824
                                         2 (bases 1 to 5381)
Pucharcos, C., Fuentes, J.J., Pritchard, M. and Estivill, X.
Direct Submission
Submitted (16-DEC-1998) Medical and Molecular Genetics Center,
Cancer Research Institute, L'Hospitalet de Llo., Avia.
Castelldefels km. 2,7, Barcelona 08907, Spain
                                                                                                                                                                                                                                                                                                    Homo sapiens
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              Location/Qualifiers
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                  (human)
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corm (ITSN) mRNA,
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PSNYVKLTTDMDPSQQ"
            GPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPT
EPPKSTALAAVCQVIGWYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF
                                                                                                                                                                                             269. .393:
                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                      'gene="ITSN"
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DB 9;

Length 5381;

ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTCGAG 0; Score 2831; Di Pred. No. 0; 0; Mismatches 475; Indels 21; 328 w

GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180 GAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCCAATATCTGGATTCATTACT GGTGATCAAGCTAGAAACTTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAG 388 448

GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT ATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATA 300 508 240

568

GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGCAGTGCCTCCCCTGGCTAAC 480 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 360 GTCATGAAAACAGCAACCAGTTGCTATTTCTAGCGCACCAGCATTTGGTATGGGAGGTATC 420 688

Qy	gg Qy	db dy	o Qy	g <i>Q</i>	D 67	Db 92	B &	р 8	Qy Db	Qy db	D Qy	සි	B &	g	D Q	р 9	g Qy	QУ
1558 ATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1617	1498 TGTCGACTGGCAACCCAGAGGCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGCCTAAGA 1557	1438 GAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGG 1497 	1378 AGGAACAAGGAGCAGGAGGACCGTGGTCCTGAAGGCAAGGAGGAGAAGACTCTGGAGTTT 1437 	1318 CTGGAAAGGCAGCACCACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAG 1377 	1258 CGGCAGCGAGAGGAGGAGGAGGAGGAGGATCGAGAGGCGCGAGAGGCCGCAAAACGGGAA 1317 	1198 CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGAGCTGGAG 1257	1138 GAGCGGTTGGCTCAGCTGGAGCGCCGAGCAGGAGAGAAAAGAGCGGGAAGCGCCAGGAG 1197	1078 GGCAGTGTGGAGCTGGAGAAGCGCCCCAAGCGCTCTTGGAGCAGCAGCAGCGCAAAGAGCAG 1137	1021 CCAGAGAAGAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGA 1077 	961 AGCTCTTCTGTGGATCÀGAGGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG 1020	901 CCAGAATACATCCCTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA 960	841 CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCGCCGTCCTGCCT 900	781 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAAACTCACTGCAGAAGAATTTATC 840	721 ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTTACCCCAGGCTCAGCTGGCT 780	661 TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA 720 	601 GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGCAGCAGCAGCTGTCCTCAGTCA 660	541 AAGAGTŤCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG 600 	481 GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA 540
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Direct Submission
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Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant Prucharcos, C., Fuentes, E., Estivill, X. and Pritchard, M. Arbones, M. L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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RKERERQEZERKROLELEKQLEKORELERGREEERRKEZERREZERRAKERELERGROLEWE
RNERGELLNQRNKEQEDIVULKAKKKTLEFELLANDKKHOLEGKLQDIRCELTTORO
EIESTNIKSRELER JEEITHLOQOLOESGOMLGRLIPERGYLEWE
RNERGELLNQRNKEQEDIVULKAKKKTLEFELLANDKKHOLEGKLQDIRCELTTORO
EIESTNIKSRELER JEEITHLOQOLOESGOMLGRLIPERGYLINDOLKOVQOMSLHROSLV
TLKRALEAKELAROHLRDOLDEVEKETRSKLOEIDIFNNOLKELREIHNKOOLOKOKS
MEAERLKOKEOGERKI IELEKOKEEAORRAGERDKOMLEHVOQDDEHORFREKLHEEERL
KREESVEKKKOGERGKOKADOKLORLIPHOLOEPAKPAVQAPWETREKGEPLTISAQENV
KVVYYRALYPFESRSHDEITIOPEDIVMVKGEWVDESQTGEPGMLGGELKGKTGWFPA
NYAEKI PENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTPNNWADFSST
WPTSTNEKPETDNWDAMAAOPSLITVEBAGOLRORSAFTPATATGSSPSVLGQGEKVE
GLQAQALYPWRASKONHLNENKNDVITVLEQDDWWWFGEVQGOKOWPKSYVKLISGP
IRKSTSNDSGSSESPASLKRVASPAKPVVSGEEFIAWTSSEPSTVGOGEKVE
GLQAQALYPWRASKONHLNENKNDVITVLEQDDWWWFGEVQGOKOWPKSYVKLISGP
IRKSTSNDSGSSESPASLKRVASPAKPVVSGEEFIAWTSSEPSTVOGGEKVE
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GPOKPLWESELLTEKEVANIFVNWKELLVGNIKLLKALEVRKKEDDDWMKGBVNEKURGVIF
PROYVKLTTDMDPSQOWGSDLHLDMLTPTEKKRQGYIHELIVTEENVVNUTGIILS
AQLPHMOPYIRFCSRQLNGAALIQAKTKTPIFEKKRGGYIHELIVTEENVVNUTGIILK
AGSINERTAWVOKIKAASELY ETTEKKKAEKAKKNKELYGETPNDPLLTQITK
PLGSSGTDKVFSFKSNLQYKMYKTPIFLNEVLVKLPTDESGDEPIFHISHIDRVYTLR
AESINERTAWVOKIKAASELY ETTEKKKAEKAKNKELYGETENDPLLTQUTEERDO
FSPDDFLGREINVADIKKDQGSKGPVTKCLLLHEVPTGEIVVRLDLQLFDEP"
GRSHGKSNPYCEVTMGSQCHITKTIQDTLNFMNSNCQPFIRDLEQEVLCITTPEERDO
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSTIRSGSGISVISSTSVDQRLPEEPV
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/product="intersectin long isoform"
/protein_id="AAD29952.1"
/db_xref="GI-808823"
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2095 ATGCAAGACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACC 2369 GCACAAGACAAGCTGGGTCGGCTTTTCCATCAACACCAAGAACCAGCTAAGCCAGCTGTC
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1978 CTGGAGCATGTGCAGCAGGAGGAGCAGCCACGCCCCGGAAACCCCACGAGAGACGAC 2034
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1858 AAGCAGAGGTCCCTGGAGGCAGCGGATGAAGCAGAAAGAGCAGGAGGGGAAGAGCCTG 1917
1798 GATGTITITCAACAACCAGGTGAAGGAACTGAGAGATACATAGCAACAGCAACTCCAG
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1618 CTFATTCCAGAGAAACKGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTG 1677
1558 ATTGCTGAAATCACCCACTTACAGCAGCACTTGCAGGAATGCTTGGAAGA 1617
1769
1438 GAGTTAGAAGCTCTGAATGACAAAAGCATCAGCTAGAAAGCTACAGGAAAATTTCAGGATATCAGG 1497
13 18 AGGAACAAGAGGAGGAGGGCACGAAGGCACAGGAGAGACTICT 1437 1649 AGAACAAAGAACAAGAGGACATAGTTGTACTGAAAGCAAAGAAAAAGACTTTGGAATTT 1708
1318 CTGGAAAGGCACGACTTGAATGGGAACGGAACGGAGCAGGAACTCCTGAATCAG 1377
1529 CUSTANG CHANGANG ANG ANG ANG ANG ANG CUSTANG CUSTANG CUSTANG ANG CUSTANG CUST
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10 / B GECAGITIGAGE TIGAKARAGCIGIC GECKAGIGGIGTITIGAGE GAGGAGGIGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG
1289 CAATTAGAAAAGAAATTACCTGTAACGTTTGAAGATAAGAAGCGGGAGAACTTTGAACGT 1348

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M., Scott, H.S.,
                                                                                                                                                               Location/Qualifiers
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CH-1211,
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short form
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                                                                                                                                                                           and Microbiology,
Switzerland
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Cy 301 GICAIGAACAGCAACCAGTGGCTATTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 360 407 GTCAIGAACAGCAACCAGTTGCTATTCTAGGCGCACCACCATTTGGTATAGGAGGATT 360 407 GTCAIGAACAGCAACCAGTTGCTATTCTAGGCACCACCATTTGGTATGGAGGATTIC 466 Qy 361 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT 420	181 287 241 347	Db 107 ATGGCTCAGTTTCCAACACCTTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG 166 Qy 61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGGATTAGCTGTAACT 120	165	SH3 SH3 SH3 27 g	misc_feature 167406 /note="encodes EH domain" misc_feature 7671936 /note="encodes EH domain" misc_feature 23242524 /note="encodes SH3 domain" misc_feature 28433019 /note="encodes SH3 domain"	TLKRALEAKELARQHINDQLDEVEKETRSKLQEIDIFNNQLKELREIHNKQOLQKQKS. MEABRIKQKEQERKI IELEKQKERAQERKADEN PRIKLHEEEKL KREBSVKKKDGEEKGKQEAQDKLGRILFHQHQEDAKPAVQAPWSTAEKGPLTISAQENV KVVYYRALVPFESRSHDEIT IQFQDIVMVGEWVDESQTGEBGWLGGELKGKTGWFPA NYABKI PENEVPAPVKPVTDSTSAPAP KLALRETPAPLAVTSSEPSTTPNNWADFSST WPTSTNEKPETDNWDAWAAQPSLTVPSAGGLQKSAFTPATATGSSPSSYVLGQGSKVE GLQAQALYPWRAKKDNHLMENKNDVITULEQQDWWWFGSVQGQKGWFPKSYVKLISGP IRKSTSMDSGSSESPASLKRVASPAAKFVVSGEEFIAMYTYESSEQGDLFFQQGDVIL VTKKDGDWMTGTVGDKAGVPFSNYVKLXDSEGGGTAGKTGSLGKKPEIAQVIASYTAT GPBQLTLAPGQLILIRKKNPGGWWBGELQARGKKRQIGWFPANYVKLLNPGTSKITPT EPPKSTALAAVCQUIGWYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF PSNIYVKLTDNDPSQO"	RNFFPGSGLPQPVLAQIWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSALPPVM KQQPVAISSAPPFGMGGIASMPPLTAVAPVPMGSIPVVGWSPTLVSSVPPYAAVPPLAN GAPPVIQPLPAFAHPAATLFKSSSFSRSGGGSQLMTKLQKAQSFDVASVPPVABWAVP QSSRLKYRQLFNSHDKTMSGHLTGPDARTILMQSSLPQAQLASIWNLSDIDQDGKLTA EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRFWRSGSGISVISSTSVDQRLPEEPV LEDEQQQLEKKLPVTFEDKKRENFFRGNLELEKRRQALLEQQRKEQERLAQLERAEQE RKERERQEQERKGQLELEKQLEKLFBELBRQALEGKLQDKEQERLAQLERAEQE RNERQELAQRNKEQEDIVVLKAKKKTLFFELBALDKKHQLEGKLQDTAGRACRELERQRQLEWG RNERGELSTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILNDQLKQVQQNSLHRDSLV
1487 1438 1547 1498 1607	1367 1318 1318 1427 1378	1138 GAGCGGTTGGCTCAGCTGGAGCGCCCAAGCAGGAGAGAAGAAGAGCGGGAAAGAGCGCCAAGAAG	Oy 1021 CCAGAGAAACHAACTGCCTGTGACATTTGAAGATAAGAAGCAGGAGAAACTTCGAAGGAGAACTTCGAAGGAGAAACTTCGAAGGAGAAACTTCGAAGGAGAAACTTCGAAGGAGAACTTTGAACGT 1186 1127 CAATTAGAAAAAGAAATTACCTGTAAACGTTTGAAGAGAAGCAGGAGAAGAAGCAG 1137 OY 1078 GGCAGTGTGGAGAAACGAAGGCCCCCAAGCGCTCTTGGAAGCAGGCGCAAAGAAGCAG 1246 OB 1187 GGCAACCTGGAAACGAAGCGAAGCTTTCTGGAACAAGGAGGAGGAG 1246 OB 1187 GGCAACCTGGAAACGAAGGAGAAGGAAGGAGAGAGAGAGA	QY 901 CCAGAATACATCCCTCCTTCAGAAGAGTTCGCTCGGCAGTGGGATGTCCGTCATA 960	Qy 781 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC 840	Oy 601 GCACAATCATTCGATGGCCAGGGCCCTCCAGCAGAATGGGCTGTCCTCAGTCA 660	Qy 481 GGGGCTCCTCCCGTCATACAGCCTCTGCCGTTTTGCGCATCCTGCAGCCACATGGCCA 540

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GCAGAAAAGATTCCAGAAAATGAAGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACA	2215 AAAGTGGTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATCACC 2274	2147 AAACTGAAAAGGAGAGAGAGAAAAAAGGTCAAAAAAGGTAAAAGGCAAAAAGGCAAAAAGGCAAAAAAGGCAAAAAAGGAAAAAA	1918 GAGTTAGAGAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGG 1977	GATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAG	1558 ATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1617
Qy 3460 Db 3587 Qy 3520 Db 3647 . Qy 3580 Db 3707 Qy 3640 Db 3767	24 24 34 34 34 34 34 34 34 34 34 34 34 34 34		0y 30 Db 31 Db 31 31 31 32 31 31 31 31 31 31 31 31 31 31 31 31 31		Db 2747 Qy 2680 Db 2807 Qy 2740 Db 2867 Qy 2860 Db 2862
3460 ATCGGGATGTACGATTACACCGCCCAGAACGATGACGACTAGCCTTCAGCAAAGGCCAG 3519	3407 ATTTTGATCCGAAAAAGAACCCAGGTGGATGTTGTGAAGCAGTGTGGAAGCACGTGGGGGGGG	GAGGGCTCTGGAACTGCTGGGAAACAGGGAGTTTAGGAAAAAACCTGAAATTGCCCAG 	TOGGGAGAAGAATTTATTGCCATGTACACTTACGAGAGTTCTGAGCAAGGAGAT TTCGGGAGAAGAATTTATTGCCATGTACACTTACGAGAGTTCTGAGCAAGGAGAT TTCGGGAGAAGAATTTATTGCCATGTACCAAGAAAGATTGTTGACTGGTGGACG TTTCAGCAAGGGGATGTGATTTTGGTTACCAAGAAAGATTGTGAGCTTAAAGATTCA CTTTCAGCAAGAGGGGATGTGATTTTTGGTTACCAAGAAAGA	TTCCC	GTTCC GTTA ACCGT

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Location/Qualifiers
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1 (bases 1 to 7247)

Guipponi, M., Scott, H.S., Chen, H., Schebesta, A., Rossier, C. and Antonarakis, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two isoforms of a human intersectin (ITSN) protein are produced brain-specific alternative splicing in a stop codon Genomics 53 (3), 369-376 (1998)
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RKERERQBEGENKRQLELEKQLEKQRELERQREEERRKETERRELERGRQLEWE
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                                                                                                                                                                                                                                                                                                                                             WPTSTNEKPETDNWDAMAAQESLTVESAJGQLAQRSAFTPATATICSSESEVULGQGEKVE
GLQAQALY PWRAKKDNHLNENKNDVI TVLEQQDDMWPGEVUQQKGWPPKS YVKLI SGP
IRKSTSMDSGSSESPASLKRVASPAAKPVVSCEEF I AMYTYESSEQGDLTFQQGDUTL
VTKKDGDWMTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPE I AQVI AS YTAT
                                                                                                                           PLGSSGTDKVFSPKSNLQYKMYKTPIFLNEVLVKLPTDPSGDEPIFHISHIDRVYTLR
AESINERTAMVQKIKAASELYIETEKKKREKAYLVRSQRATGIGRLMVNVVEGIELKP
CRSHGKSNPYCEVTMGSQCHITKTIQDTLNPKMNSNCQFFIRDLEQEVLCITVFERDQ
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                 note="encodes
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GCACAGTCATTTGATGTGGCCAGTGTCCCACCAGTGGCAGAGTGGGCTGTTCCTCAGTCA
                                                                                          AAGAGTTCTTCCTTTAGTAGATCTGGTCCAGGGTCACAACTAAACACTAAATTACAAAAG
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J. Biol. Chem.
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                                                                 Okamoto, M., Schoch, S. and Sudhof, T.C. EHSH1/intersectin, a protein that contains EH and SH3 domains binds to dynamin and SNAP-25. A protein connection between
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J. Biol. Chem. 274 (26), 18446-18454 (1999)
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Okamoto,M., Schoch,S. and Sudhof,T.C.
Direct Submission
Submitted (02-MAR-1999) Center for Basic Neuroscience
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                                        GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT
                                                                                                               GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT
                                                                                                                                                                                                                                                                                                                                        GGTGATCAAGCGAAGCTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA
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                                                                                                                                                                 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCCT
                                                                                                                                                                                                                                                                                                             GGTGATCAAGCAAGGAACTTCTTTTTCCAATCTGGGTTACCTCAGCCCGTCTTAGCACAA
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Pred. No. 0;
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Length

Gaps

180

160 120 100 60

420 400

340 300 280 240 220

421 GGALTGTTCCCCCCTTAGTACTCCTCTCCCCCCAGGAGCAGCAGCCCCCCCTGCCTAGC 480 461 GGALTGTTCCCCCCCTTAGTATCTCTTCTCCTCCCCTTAGCAACCAGCCCCCCCTGCCTAAGC 480 461 GGALTGTTCCCCCCCTTAGTATCTCTCTCTCCTCCCCTTGCTAAGC 520 461 GGALTGTTCCCCCCCCTTAGTATCTCTCTCTCTCTCTCTCTCTC
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1 1	CAATGA 3481	3425 CTCTTCCCGTCCAATTATGTGAAGCTGACCACAGACATGGACCCCAGCCAG	D
misc feature	TAATGA 3642	6 CTCTTCCCATCCAATTATGTAAAGCTGA	
misc_feature			
misc_feature			
	AAGTTGGG 3585	3526 AACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAAAGTCAGTGGGCAAGTTGGG	Q
		3305 ATGTACGATTACACCGCGCAGAATGACGATGAGCTAGCCTTCAGCAAAAGGCCAGATCATC	Db 4
		3245 ATCACCCCAACTGAGCTACCCAAGACCGCAGTGCCAGCCA	
	TGATCGGG 3465	3406 ATCACCCCAACTGAGCTACCCAAGACCGCAGTGCAGCCAGC	γ ο
	 CAAGCAAA 3244	3185 CGCCAGATAGGGTGGTTCCCAGCAAATTATGTCAAACTTCTAAGCCCTGGAACAAGCAAA	Db
	СААССААА 3405	3346 CGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAAGCCCCGGGAACAAGCAAG	99
	 GGAAAAAG 3184	3125 ATCCGAAAAAAGAACCCCGGTGGATGGTGGGAAGAACTACAAGCTCGAGGGAAAAAG	Db s
	эссалалас зз45	3286 ATCCGGAAAAAGAACCCAGGTGGATGGTGGGAAGGAGGAACTGCAAGCTCGAGGGAAAAAG	Q
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	TGATTCTG 3285	3226 GCTTCCTACGCTGCTACTGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTG	Qy :
	 AGGTCATT 3064	3047GANATCGCCCAGGTCATT	Db 3
	AGGTTATT 3225	3166 TCTGGAACTGCTGGGAAAACAGGGAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATT	Q S
	3046	3047	Db
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	3046	3047	Db
CDS	CGGGAACG 3105	3046 TTTCAGCAAGGGGATGTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGGAACG	Qy
3	3046	3038 CCTGGAGAA	Db 3
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٠	 ATACTGGC 2977	2918 AAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC	Db
	ATACTGGC 2925	2866 AAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC	8
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	GGTTCCCC 2865	2806 CTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	Q Y
RS		2798 CCCTGGAGAGCCAAAAAAGACAACCACTTAAATTTTAACAAAAGTGATGTCATCACCGTT	
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		2738 CCTTCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTCCAAGCACAAGCCCTGTAT	
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DEFINITION Xenopus 1		2626 AGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCC	S S
	CTGTACCC 2677	2618 GAGAAACCAGAAACGGACAACTGGGACACGTGGGCGGCTCAGCCTTCTCTGACTGTACCC	망

RESULT 9 AF032118

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1,N.G., Hardisc
Submission
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Chem. 273 (47), 31401-31407 (1998)
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a; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed (30-OCT-1997) Pharmacology, University of Wisconsin, 1300
ity Ave, Madison, WI 53706-1532, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus laevis"
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193. _4005
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/note="EH domain and SH3 domain containing protein;
similar to intersectin binding proteins Ibp1, encoded
GenBank Accession Number AF057285, and Ibp2, encoded b
GenBank Accession Number AF057286, and mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAPAVIQSHPAFAHSATLPKSSSFGRSVAGSQINTKLQKAQSFDVPAPPLVVEWAVPS
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1975 TGGCTGGAGCATGTGCAGCAGGAGGAGGAGCAGCCCCCCGGAAACCCCACGAGGAG	Qy S	1024 TITATATTAGCTATGCACTTAATAGATGTGGCCARGTCTGGCCAGCCACTTCCTCCAATC 1083 895 CTGCCTCCAGAATACATCCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCC 954	. 6 B
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1855 CAGARGCAGARGETCCCTGGAGGCAGCCGCACTGGAGCAGGAAGAGCAGGAAGAGACGAAAAAACCGAGAAACAGCCTGGAAACAGCTGGAAACAGCTGAGAAAGAGCTGGAACGAAAAAACC	B &	775 CTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAA 834 	유 성
1795 ATTGATGTTTTCAACAACCAGCTGAAGGAACTGGAGGAGATACATAGCAACAACCAGCTGAAGGAACTGAGAGAATTGTACAACAAGAAGAGCAGTTC 1984 ATCGACGTATTTAATAACCAATTAAAGGAACTGAGAGAATTGTACAACAAGAGCAGCAGTTC	5 A	715 CACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCCAGGCTCAG 774	유 성
1735 CAGCAGCTCCGGAGCAGCTGGACGAGGTGGAGAGACCAGGTCAAAGCTGCAGAG 1794	₽ &	655 CAGTCATCAAGGCTGAAATACAGGCAGGTTATTCAACAGCCACGACAAAACTATGAGTGGA 714	B 8
1675 TIGCATAGAGACTIGCTTCTTACCCTCAAAAGAGCTTGGAAAGAACTAGCTGGCCGG	, B &	595 CAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCCCCAGCAGCAGAATGGGCTGTGCCT 654	B 8
804	P &	535 TGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTA 594	유 성
155 AGANTIGCTGANATCACCCACTTACAGCAGCTGCAGGAATCCTCAGCAATGCTTGGA 1614) B &	475 GCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCGTTTGCGCATCCTGCAGCCACA 534	음 성
1684 CGGTGTCGCCTACTACTCAACGGCACGAAATAGAAAAGCACTAACAAATCCAGGGAACTG 1743	р <i>2</i>	415 GTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTG 474	음 성
1 13 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1	S & &	355 GGGATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCCAATGGGCTCCATTCCA 414	<u> </u>
13.5 CHARGERAL TANGGARGA CANGAGA CANGGARGA CANGAGARGA CANGGARGA CA) B &	301 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGA 354	음 성
	? B £	241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300	음 성
TABLE TABL	S B 8	181 ATATGGGCGTAGCGGACATGAATAACGATGGAAGGATGGAT	음 성
	S B &	121 GGTGATCAAGCGAGGAACTTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180 	음 성
1135 CAGGAGGGGCAAGGGGCAGGAGGAGGAGGAGGAGGAGGAG	S B 5	61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 120 	음 성
10/3 CHAGGLAGICIGAGEL IGHAGHAGUGCUCCHARCUCIC I IGHAGCHGCACUGCARAGAG	S B 8	1 ATGGCTCAGTTTCCCACACCTTTCCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 60 	유 <i>성</i>
1015 CAGCAGCCAGAGAAAACTCCCTGTGACATTTCAAGATAAGACGGGAGAACTTTCGAG 1074	}	Query Match 55.7%; Score 2027.6; DB 5; Length 4103; Best Local Similarity 73.6%; Pred. No. 0; Matches 2685; Conservative 4; Mismatches 918; Indels 39; Gaps 7;	
955 GTCATAAGCTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAG 1014	B & 8	/note= 	68 88 89
1084 CTGCCTCCAGAGTATATTCCCCCATCTTTTAGAAGAGTTCGATCAGGGAGTGGGTTATCC	D b	misc feature 33643558	

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OS Homo sapiens (human)
PN JP 2002017375-A/2599
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZU
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC 112N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
                                                                  10,
PC C12
Primer
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1 (bases 1 to 2131)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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                                                                                                                                                                                                                                                                                                                                   Primer for synthesizing full-length cDNA and Patent: JP 2002017375-A 2599 22-JAN-2002;
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ner for synthesizing full-length cDNA and use thereof FH
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
Location/Qualifiers
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181 ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATCAAGTGGAATTTTCCATA 240		GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT	TTTCCCACACCTTTTGGTGGCAGACTGGATGTCTGGGCCATAACTGTGGAG 60	Query Match 40.7%; Score 1483.8; DB 9; Length 2131; Best Local Similarity 86.0%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 267; Indels 3; Gaps 1;	/dev_stage="embryo, 10 weeks" /note="cloning vector: pME188FL3" 694 a 469 c 526 g 442.t	/db_xref="taxon:9606" /db_xref="taxon:9606" /clone="HEMBA1004110" /tissue_type="whole embryo, mainly head" /clone="jb="WEMBA1"		Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).	(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction:	Isogal,T. and Otsuki,T. Direct Submission Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan	NEDO human cDNA sequencing project Unpublished 2 (bases 1 to 2131)	Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Makamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	4.1 app: pier pier	Homo sapiens cDNA FLJ90073 fis, clone HEMBA1004110, highly similar to Homo sapiens intersectin short form mRNA. AK074554
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FEATURES SOURCE BASE COUNT	TITLE JOURNAL COMMENT	RESULT 12 BD158570 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	B 8		8 8 8 8	A A		용 성	0 dd	Db 1
CI2N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers (347)(2131). Location/Qualifiers 12131 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /db_xref="taxon:9606" /db_xref="taxon:9606" /db_xref="taxon:9606" /db_xref="taxon:9606"	Ota, T., 1809a1, T., NISDIKAWA, T., HAYASDI, K., SAILO, K., YAMAMOTO, J., Ishi, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 13413 09-JUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/13413 PD 09-JUL-2002 PF 28-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI	BD158570 BD158570 BD158570 BD158570.1 G1:27864328 JP 2002191363-A/13413. Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Veri Mammalia; Butheria; Primates; Catarrhini; H 1 (bases 1 to 2131)	1918 GAGTTAG 1924 2125 GAATTAG 2131	AAGCAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAAGAGCAGGAGAGAGA	1738 CAGCTCCGGGAGCAGCTGGACGAGGTGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATT 1797	1678 CATAGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAG 1737 	8 CTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTG 1 	1558 ATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1617	1498 TGTCGACTGGCAACCCAGAGGCAAGAATTGAGAGCACGAACAAGTCTAGAGAGCTAAGA 1557	1645 GAATTAGAAGCTCTAAATGATAAAAAGCATCAACTAGAAGGGAAACTTCAAGATATCAGA 1704
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                            Homo sapiens cDNA FLJ14940 fis, clone PLACE1010942, highly to Homo sapiens intersectin long isoform (ITSN) mRNA.

AK027846

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AK027846 1 GI:14042823

oligo capping; fis (full insert sequence).

Homo sapiens (human)
    Eukaryota; Metazoa; Chordata;
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                          sapiens
  Craniata; Vertebrata;
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  Euteleostomi;
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highly similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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Isogai,T. and Otsuki,T.
Direct Submission
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GGGGCTCCCCTGTTATACAACCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCCA
                            GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA
                                                                                                      GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCCTGGCTAAC
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/clone="PLACE1010942"
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                     ATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1617
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Best Local Similarity
Matches 1227; Conserv
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3071
PN JP 2002017375-A/3071
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
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PI ISHII,
PI TURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIIC
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
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1 (bases 1 to 1676)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCCTGGCTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTTCCATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180
GAGCGGTTGGCTCAGCTGGAGCGCGCGCGAGCAGGAGAGGAAAGAGCGGGAGCGCCAGGAG
                                                                                                     GGCAGTGTGGAGCTGGAGAAGCGCCCCAAGCGCTCTTGGAGCAGCAGCAGCAAAAGAGAGCAG 1137
                                                                                                                                                     CAATTAGAAAAGAAATTACCTGTAACGTTTGAAGATAAGAAGCGGGAGAACTTTGAACGT
                                                                                                                                                                                                                                                  AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG 1020
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Best Local Similarity
Matches 1227; Conserv
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264
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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
MEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa, Natsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK075290.1 GI:22761283 oligo capping; fis (full insert Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK075290 1676 bp mRNA linear Homo sapiens cDNA FLJ90809 fis, clone Y79AA1000778, to Homo sapiens intersectin long form mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1676)
Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEDO human cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG
                    ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG
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                                                                                                                                                                                 485
                                                                               Conservative
                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="y799A11000778"
/cell_line="Y79"
/cell_type="retinoblastoma"
/clone_lib="Y79AA1"
/note="cloning vector: pME185
a 381 c 458 g 352 t
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                                                                                               30.3%;
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0; Mismatches 183;
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1197	138 GAGCGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAGAGGAAAGAGCGGGA	
1137 1403	1078 GGCAGTGTGGAGCTGGAGAAGCGCCCGCCAAGCGCTCTTGGAGCAGCAGCAGCGCAAAGAGCAG	
1077 1343	TGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGA 	
1020 1283	961 AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG	
960 1223	CAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA TAGAAGAGTTCGATCTGGCAGTGGTATATCTGTCATA	
900	GTCAGCCACTGCCGCCCGTCCTGCCT	
840 1103	81 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC	
780 1043	AGGCTCAGCTGGCT AGGCTCAGCTGGCT	
720 983	61 TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAACTATGAGTGGACACTTA	
660 923	01 GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA	
600 863	1 AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG	
540 803	81 GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCCTTTTGCGCATCCTGCAGCCACATGGCCA	
480 743	1 GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC	
420 683	1 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT	
360 623	01 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT	
300 563	41 GCCATGAAGCITATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT	
240 503	81 ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATCGATC	
180 443	1 GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA	
120 383	61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGGATTTATTACT	

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	AGAAACAAAGAACAAGACATAGTTGTACTG 1676	1644	문
	AGGAACAAGGAGGAGGGCACCGTGGTCCTG 1410	1378	Ş
Ş-	CTTGAAAGGCAACGACAACTTGAGTGGGAACGGAATCGAAGGCAAGAACTACTAAAI	1584	문
=ğ	CTGGAAAGGCAGCGACAACTTGAATGGGAACGGAAACCGGAGACAGGAACTCCTGAATCAG 1377	1318	Ş
8-	CGGCAGAGAGAGGAGGAGGAAAGAAATTGAGAGGCGAGAGGCTGCAAAAACGGGAA 1583	1524	В
-8 -8	CGGCAGCGAGAGGAGGAGGAGGAAGGAAGACGGGAAAACGGGAA 1317	1258	Ş
<u>۾</u>	CAAGAGCGCAAAAGACACTGGAACTGGAAGCAGCAACTGGAAAAGCAGCGGGAGCTAGAA 1523	1464	망
-8 -8	CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCGGGAGCTGGAG 1257	1198	ş
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Search completed: December 4, 2003, 21:34:19 Job time : 8623.82 Becs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pland is derived by analysis of the total score distribution.
         5060
3886.4
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Match
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1: /SIDS1/gcgdata/geneseg/genesegn-emb1/NA1980.DAT:*

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13:
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         99.5
76.4
73.2
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Copyright (c) 1993 - 2003 Compugen
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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Mouse Esel full le Mouse Eselt CDNA s Mouse Eselt coding Mouse Eselt coding Human SH3DIA cDNA Human SH3DIA cDNA Human SH3DIA cDNA DNA encoding novel
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AAZ39008
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Mouse secreted exp	AAA43984	21	229	3.9	198.8	45
Human adipocyte Se	7	25	701	4.1	206	44
DNA encoding novel	AAS84759	23	395	4.1	210.8	43
Human secreted exp	AAA44038	21	346	4.9	250	42
Human SH3P18 gene.	AAT39796	17	747	.5.1	258	41
Human cDNA clone (AAH03435	22	831	ហ ហ	281	40
cDNA encoding nove	AAS27090	22	4210	6.5	331.4	39
DNA encoding novel	ABK43586	23	3746	6.5	331.4	38
	AAT39799	17	2873	6.6	333.2	37
	AAI80000	22	548	7.0	356	36
cDNA sequen	AAH15260	22	1329	7.6	387.4	ω S
Human cDNA clone (AAH08146	22	676	8.0	405	34
m.	ABK43814	23	568	8.0	406	33
cDNA encoding nove	AAS31621	22	568	8.0	406	32
Human polynucleoti	AAI63919	22	568	8.0	406	31
Ovarian carcinoma	ABN72656	24	2017	9.5	484.8	30
	AAA69762	21	2017	9.5	484.8	29
Human adipocyte Se	ACA57641	25	677	10.1	513.8	28
Human cDNA clone r	AAK93179	22	877	12.0	611.6	27
Human cDNA 5'-end	AAK91610	22	877	12.0	611.6	26
DNA encoding molec	AAS02055	22	4447	13.0	659	25
Mouse Ese2 coding	AAZ39011	21	3593	13.1	666.6	24
	AAZ39027	21	4975	13.3	677	23
Mouse Ese2L cDNA s	AAZ39026	21	6014	13.5	687.6	22
Mouse Esež full le	AAZ39010	21	4625	13.5	687.6	21
Human polynucleoti	AAK52332	22	6103	14.2	724.2	20
Allergic disease e	AAL47247	24	5828	14.3	726.4	19
Human SH3P17 gene.	AAT39795	17	1389	16.9	858	18
	ABQ55007	24	2067	17.3	881.8	17
Human cDNA, SEQ ID	AAK94611	22	1676	24.6	1249.2	16
 DNA encoding novel 	AAS84762	23	2874	25.4	1291.4	15
	AAZ34574	20	3231	27.4	1395.4	14
	AAH16578	22	2131	27.6	1404.2	13
SH3D1	AAZ34573	20	2079	31.2	1584.4	12
Human full-length	AAK94139	22	2131	31.7	1610	11
DNA encoding novel	ABK43498	23	3319	42.1	2140.8	10
Human polynucleoti	AAI63825	22	3466	43.1	2188.8	9

ALIGNMENTS

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WPI; 2000-052802/04
                                                                                                                                                        Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
                  Egan SE,
                                                       27-APR-1998;
05-FEB-1999;
                                                                                                    04-NOV-1999.
                                                                                                                       WO9955728-A2.
                                                                                                                                       Mus sp
                                                                                 27-APR-1999;
                                    (HSCR-) HSC RES & DEV LP.
                 Wang W, Sengar A;
                                                      98CA-2230201
99US-0118739
                                                                                 99WO-CA00375
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Mouse Esel full length cDNA sequence.

28-FEB-2000 (first entry)

AAZ39008;

AAZ39008 standard; cDNA; 5082 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes mouse Esel. The present invention CC specifically describes mammalian Esel and 2 proteins (I) and their splice CC variants (Bse = BH-domain and SH3-domain regulator of endocytosis). (I) CC are involved in regulation of clathrin-mediated endocytosis (as a complex CC with Espl5 protein), vesicular trafficking and actin cytoskeleton. CC denerally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular CC function. Particularly overrexpression of Esel is used to block CC clathrin-mediated endocytosis in vivo or in cell cultures, while CC daministration of (I) is used to promote endocytosis of selected cells. CC (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent CC unplex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal compounds can be treated include cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e\cdot g\cdot for treating cancer or preventing viral
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                                  CAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTC
                                                  CAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTC
                                                                                               GGTGAACGTAATAGAACCATGGCTCAGTTTCCCCACACCTTTCGGTGGTAGCCTGGATGTC
                                                                                                                                                                                                                                                                                                              GGTGAACGTAATAGAACCATGGCTCAGTTTCCCCACACCTTTCGGTGGTAGCCTGGATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signalling, tissue development or synaptic transmission.
                                                                                                                                                            ATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTT
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AAZ39024 standard; cDNA; 5738

28-FEB-2000 (first entry)

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Mouse EselL cDNA sequence

Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.

de an

WO9955728-A2

04-NOV-1999

27-APR-1999; 99WO-CA00375.

27-APR-1998; 05-FEB-1999; 98CA-2230201. 99US-0118739.

SE, ξ, Sengar A,

RES & DEV

WPI; 2000-052802/04. P-PSDB; AAY57449.

New nucleic acid encoding Esel and 2 proteins, for treating cancer ę involved in regulation or preventing viral

Claim 6; Page 56-59; 99pp; English

ARESULT 2
ARESUL The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-cc mediated endocytosis (as a complex with Espl5 protein) vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polymucleotide; agents that downregulate cc expression of Ese genes or antagonists of an Ese binding partner are CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of CC Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal CC proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be cused to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC cancer; abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Eseil CDNA sequence.

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960 AACTATGAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTT 1019 	900 ATGGGCTGTGCCTCAGTCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAA 959	840 AAACACTAÁGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGCAGA 899	780 TCCTGCAGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATT 839	720 AGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTGC	660 GGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGC 719	600 ATTTGGTATAGGAGGGATTGCTAGCATGCCACCCACTCACAGCTGTTGCTCCTGTGCCAAT 659	540 CCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGC 599	480 TCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCT 539	420 TCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGA 479 	360 GATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTTT	300 CTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCC 359	240 AGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGT 299	180 CACTGATTTGTGTGAGGGGGGGGCGCGCGCGCGCGCGGAGATGAGGCGTCGATCAGCA 239	120 GCGGGCGGGATGGTGTGCGGGCTGCGGACTCCGGCGTTCCTCGCGCGGCGTGCGGGCTG 179	60 GGCGGCTCGCAAGGGAGCATCCCGAGCCGGGCTCCCGGGACGGCAGGCA	1 CGGCACGAGGAGGAGGGGCGCGCGCGCGCGCGCGCGCGC	ry Match 76.4%; Score 3886.4; DB 21; Length 5738; It Local Similarity 99.9%; Pred. No. 0; Ches 3898; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	equence 5738 BP; 1556 A; 1456 C; 1613 G; 1113 T; 0 other;
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28-FEB-2000

(first

entry)

Mouse Esel coding sequence

AAZ39029
AAZ39029
ID AAZ3
XX AAZ3
AC AAZ3
XX BACA
DT 28-F
XX MOUS
KW MOUS
KW EH-d
KW EH-d
KW EH-d
KW MUS
KW EH-d
KW MUS
KW WO99
XX WO99 Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.

WO9955728-A2

27-APR-1999; 99WO-CA00375.

27-APR-1998; 05-FEB-1999; 98CA-2230201. 99US-0118739.

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mutants); (i) specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. CC (Ant) agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or abnormal cell division or signalling, tissue development or synaptic transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 3723;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton.

Generally (I) (or its (ant) agonists, mimetics, fragments and inactive denerally (I) (or its (ant) agonists, mimetics, fragments and inactive denerally (I) (or its (ant) agonists (Ab); sequences antisense to the (I)
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                                                                                                                                                                                                     CC The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocycosis). (I) are involved in regulation of clathrin-cc mediated endocytosis (as a complex with Espl5 protein), vesicular cc trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); esequences antisense to the (I) polynucleotide; agents that downregulate cc expression of Ese genes or antagonists of an Ese binding partner are cc used to treat diseases associated with undesirable endocytosis and cresulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to propress abnormal cc groliferation of cells that can be stimulated to promote endocytosis of cc selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal cc proliferation of cells that can be stimulated to proliferate by a growth cf actor receptor; and similar compounds (also inactive Ese mutants) can be cused to prevent viral infection. Endocytosis may also be regulated, in compounds (Ese compounds) complex, then binding conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal cc receptor signalling, tissue development or synaptic transmission. The presents mouse Esell coding sequence.
                                                                                    Query Match
Best Local Similarity
Matches 3640; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
                                                                                                                                                                          Sequence
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3559 CCACGTGGATGGTGGGAAGGAAACTGCAAGCTCGAGGAAAAAGCGCCAGATAGGGTGG 3618	8	79 GTATATTAC	, &
3499 ACTEGITOCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAAGAAC 3300 3241 ACTGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAAAGAAC 3300	Db Q	2419 CCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGAGAGTGTAAAAGTG 2478 .	음 성
	D 2	2359 GACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCA 2418	유왕
	O B 1	2299 AAGAGGGAAGACAGTGTCAGGAAGAAGGAGGGCGGAAGAGAGAG	B 8
3319 GEAGTETTECCTTATCTATCTGAGGCTTAAAGATTCAGAGGCCTCTGGAACTGCTGGG 3438	o	2239 GAGCATGTGCAGCAGGAGGAGGAGCCACGCCCCCGGAAACCCCACGAGGAG	B 8
3259 ATTGCCATGTACACATACGAGAGTTCTGAGCAAGGGATTTAACCTTTCAGCAAGGGAT 3318	? B &	179 TTAGAGAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAG(B <i>&</i>
3199 GCTAGTCTAAAGAAGTGGCTTCCCCGGCCGCCAGCCAGCAGCATCCCCGGAGAAGAGTTT 3258	Db Qy	2119 CAGAGGTCCCTGGAGGCAGGCGCGACTGAAGCAGAAAGAA	유 성
CTCATTTCAGGGCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCT 	- P Q	2059 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAG 2118	당 왕
30/9 ATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	. B &	1999 CTCCGGGAGCAGCTGGACGAGGTGGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGAT 2058	B &
2761 AAAGACCACCITAAAIIIIAAAAAAAGIGACGTCATCACCGITCIGGAACAGCAAGAC 2076 2761 AAAGACAACCACTTAAAITTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAC 2820	D 4	1939 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAAGAGCAAAGGAGCTGGCCCGGCAGCAG 1998	당 성
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265 GGCANGASTIANCETIACCCCNACCANGCCCTUSTICCCCTCCCCATCICCCCTCCCATCICCCCTCCCCATCICCCCTCCCCATCICCCCTCCCCATCICCCCTCCCCATCICCCCATCICCCCATCICCCCATCICCCCTCCCCATCICCCCATCICCCCATCICCCCATCICCCCATCICCCCATCICCCCATCICCCCATCICCCATCICCCATCICCCATCICCATCICCATCICCATCICCATCATCICCATCICCATCATCATCATCATCATCATCATCATCATCATCATCAT) D 4	1819 GCTGAAATCACCCACTTACAGCAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTT 1878	B 성
2839 GACAACTEGGATACGIGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGCCAGITA 2898 2839 GACAACTEGGATACGIGGGCGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGCCAGTTA 2640 2581 GACAACTGGGATACGTGGGCGCTCAGCCTCTCTCTGACCGTACCTAGTGCTGGCCAGTTA 2640	? B &	1759 CGACTGGCAACCCCAGAGGCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGACTT 1818 	B 성
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2/19 GCTCTGGCTGAGACCCCTGCTCTTTTGCAGTGACCTTTTTCTAAGCCCTCCACAACCCCC 2/10 2/461 GCTCTGCCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTTCTGAGCCCTCCACAACCCCC 2520 2/461 GCTCTGCCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTTTTTGAGCCCTTCCACAACCCCC 2520	; p &	1639 AACAAGGAGGAGGGGACGGTGGTCCTGAAGGCAAGGAAGAACTCTGGAGTTTGAG 1698 	문 <i>원</i>
GREGITICCACTCCAGCCAAACCAGTGACCGATCTGACATCTGACCCCTGCCCCCAAACTGACGATCTGACATCTGACATCTGCCCCTGCCCCCAAACTGACGATCTGACATCTGCCCCTGCCCCCAAACTGACGATCTGACATCTGCCCCCTGCCCCCAAACTGACGATCTGACATCTGCCCCCTGCCACAACTGACGATCTGACATCTGCCCCTGCCACAACTGACGATCTGACATCTGCACATCTGACATCTATCT	5 B 8	1579 GAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAGAGG 1638	B 8
GAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATTCCAGAAAAT	Qу	.519 CAGCGAGAGGAGGAGGAGGAAGGAAGATCGAGAGGCGCGAAGGCCGCAAAACGGGAACTG 15	B 성
2339 CCAGGAGATATAGTCATIGGTGGATGAAAGCCAGACTGGAGGAGGCCAGGATGGCTTGGAGGA 2598	da Ab	1459 GAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGCAGCGGGAGCTGGAGCGG 1518 	B 8
		1399 CGGTTGGCTCAGCTGGAGCGCCGAGCAGGAGAGGAGAGG	B 8

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           This is the nucleotide sequence of full-length cDNA (clone 21) corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the
                                                                                                                                                                                  Nucleic acid from the human the diagnosis and treatment
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83.7%;
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progress or megakaryoctyic abnormality, myeloproliferative dihaematopoietic disorder, platelet disorder or leukaemia; and tractment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a nucleic acid that expresses SH3DIA or its antisense nucleic a abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lisencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, tromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural Sequencing of 5 different sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of disorder, acid

GAGGAGGAGTGGAGCGCGCGGGAGGGCGCAGCTTGGTTGCTCCGTAGTACGGCGGCT 5458 BP; 1671 A; 1201 C; 1307 G; 1279 T; 0 other; GAGAAGAGTGGAGGCCCAGGGGAGGGAGCCTAGCTTGGTTGCTCCGTAGTACGGCGGCT Score 3529.4; Pred. No. 0; Mismatches 766; Indels B 20; Length 69; Gaps 126 84 66 22

CACACTTCCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTTGG GGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTC GGGATGGTGTGCGCGGCTGCCGGACTCGGCGTTCCTCGC-GCGGCGTGCGGGCTGCACTGA CATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCC GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC CATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGC TATAGGAGGGATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTC TGCACTTCCCCCTGTCATGAAACAGCAACCAGTTGCTATTTCTAGCGCACCAGCATTTGG TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC ACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGC TTTGTCCCTGGGGCGCAGCGCGGACCCGGCCGGAGATGAGGCGTCGATTAGCAAGGTAA TTTGTGTGAGGGGGGGGCGCGCGCACCCGGCGAGATGAGGCGTCGATCAGCAAGGTGA GGGATGGTGTGCGGGTTGCGGCTCCTGCGTCCCTCCCAGCGGCGCGCGTGAGCGGCACTGA GACAGAGAGGCGGGCG 673 665 253 185 725 613 509 553 545 493 485 433 425 373 365 313 305 245 193 133

	TCAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAATTGAGAGCACGAACAAGTC	GACTCTGGAGTTGAGGTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACT 	ACTCCTGAATCAGAGGAACAAGAGCAGGAGGACCGTGGTCCTGAAGGCAAGGAGGA 1 	63 CGCAAAACGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGA 1 	503	1443 GGAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGAGAAGCAGCTGGAGAAAGCA 1502 	1383 GCGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCCGGCCG		266 GGATGAGCAGCCAGAGAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGA 13	6 GATGICCGTCATAAGCICITCTICTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGA	146 GCCCGTCCTGCCTCCAGAATACATCCCTCCTTCAGAAGAGTTCGCTCCGGCAGTGG	086	GGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGC	GAGTGGACAC	TGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTAT	TAAGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGC	AGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACAC	726 TCCCCTGGCTAACGGGCTCCTCCCGTCATACAGCCTCTGCCTGC
	Db Qy	ДУ	Qу	Db Qy	B &	B &	D Qy	D QY	Db Qy	B &	B &	B &	db Qy	B &	B &	dg Qy	VQ	dg Qy
2865 GCCTTCTCTGACCGTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGC 2924	GTGGCCCAGCAGCTCAAACGAAAGCAGAAACGGACAACTGGGATACGTGGGCGGCTCA	2745 GCCAGTGACCTCTTCTGAGCCCTCCACAACCCCCAACAACTGGGCAGACTTCAGTTCCAC 2804	2685 GACCGATCTGACATCTGCCCCTGCCCCCAAACTGGCTCTGCGTGAGACCCCTGCTCCTTT 2744	2625 CCCTGCAAACTATGCAGAAAAGATTCCAGAAAATGAGGTTCCCACTCCAGCCAAACCAGT 2684		20 CGATGAGATCACCATCCAGCCAGGAGATAACTCAT		GCCAGCCAGGCACCCTGGTCTACCACKGAAAAGGCCGGCTTACCATTTCTGC 	AGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGC					2043 GCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGA	GCTGGCCCGGCAGCAGCTCCGGAGCAGCTGGACGAGAGAGA			1803 TAGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCA 1862

. B & B & B

AGTCAATGAACAAGTGGGCCTCTCCCATCAATTATGTGAAGCTGACCACAAGACATGGA 3913 CCCCAGCCAGCAATGAATCATTATGTTGTCCATCCCCCCCC
AAGCCCCGGAACAAGATCACCCCAACTGAGCTACCCAAGACCGCAGCGCAGCGAGCG
TCCTGGGCAGCTGATTCTGATCCGGAAAAGAACCCAGGTGGATGGTGGGAAGGAGAACT 3584
GCTTAAAGATTCAGACGCTCTGGAACTGCTCCGAAAACAGGGAGTTTAGGAAAAAAACC 3464
TGAGCAAGGAGATTTAACCTTTCAGCAAGGGGATGTGATTTTGGTTACCAAGAAAGA
AAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTGGAGGAAGTTCAAGG 3104
ACAAGCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAGACAACCACTTAAATTTTAACAA 3044
CACAGCCACTGGCTCCTCCCCATCTCCCGGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCT 2984

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cc involving the megakaryocytic lineage. The SHIJDIA gene maps to the convergence of the megakaryocytic lineage. The SHIJDIA gene maps to the convergence of different sizes of cDNA clone from foetal brain convergence of different sizes of cDNA clone from foetal brain convergence of the state of cDNA clone from foetal brain convergence of the state of cDNA clone from foetal brain convergence of the state of cDNA clone from foetal brain convergence of the diagnosis and treatment of the convergence of the state of the diagnosis and treatment of convergence of the progress and adequacy of a treatment; monitoring tumour risk convergence of a subject (including a prenatal subject) having convergence of a subject (including a prenatal subject) having convergence of the progress of a subject (including a prenatal subject) having convergence of a subject (including a prenatal subject) having convergence of a subject (including a prenatal subject) having convergence of the subject of a subject (including a prenatal subject) having convergence of the convergence of the subject of the convergence of the convergence of the subject of the convergence of the convergenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid from the human SH3D1A gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-633829/54.
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                                                                                                                                                                        GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA
                                                                                                                                                                                                                                                                                AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG
                                                                                                                                                                                                                                                                                                                                                                                             GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA
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                                                                                            TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA
                                                                                                                                                                                                                                                                                                                                                          GGGGCTCCCCCTGTTATACAACCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAGCATGCCACCGCTTACAGCTGTTGCTCCAGTGCCAATGGGATCCATTCCAGTTGTT
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                                        TCAAGACTGAAATACAGGCAATTATTCAATAGTCATGACAAAACTATGAGTGGACACTTA
                                                                                                                                             GCACAGTCATTTGATGTGGCCAGTGTCCCACCAGTGGCAGAG
                                                                                                                                                                                                                                                     AAGAGTTCTTCCTTTAGTAGATCTGGTCCAGGGTCACAACTAAACACTAAATTACAAAAG
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3133 GTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAA 3192		2056 GATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAG 2115	~
3073 CAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	Qy Db	1996 CAGCTCCGGGAGCAGCTGGACGAGGTGGAGAGAGAGACAGGTCAAAGCTGCAGGAGATT 2055	σ <
	. pb	1936 CATAGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAG 1995	σ <
2953 GTCCTGGGCCAGGGTGAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTGGAGA 3012	QY Db	1876 CTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTG 1935	σ <
3 CAGTTACGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACCAGCGCTCTCCC	D D	1816 ATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1875 	σ <
GAPACGGACACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGC	Qγ		σ <
2773 ACCCCCAACAACTGGGCAGACTTCAGTTCCACCTGGCCCAGCAGCTCAAACGAGAAGCCA 2832	Qy Db	1696 GAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGG 1755 	0 4
	Qy Db	1636 AGGAACAAGGAGCAGGAGGCACGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTT 1695	σ <
GAAAATGAGITICCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCCTGCCCCCG [db Qy	1576 CTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAG 1635	0 <
GANGSACHGC LIGHANGSANGAC GGASA IGGTECCC IGCANACTATIGCAGANANGATECCA	D 64	1516 CGGCAGCGAGAGGAGGAGGAAGGAAGATCGAGAGGCGCGAAGCCGCAAAACGGGAA 1575 	σ <
A TICCAGC CAGGARGA LAIRAGT CATGGATGAAAGC CAGACT GGAGAACCCAGGAT IGGCTT	?	1456 CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAACCAGCGGGAGCTGGAG 1515	σ <
AMAGINGIA IA I ACCUMONGCI GIACCCI I INAMI CAMANDI CACUAI INAMI CAC 	. פ	1396 GAGCGGTTGGCTCAGCTGGAGCGCCGCCGAGCAGGAGAGGAGAAGAGCGCGGAGCCCAGGAG 1455	σ <
CAGGCACCCTGGTCTACCACAGAAAAGCCCGGTTACCATTTCTGCACAGAGAGTGTA	ς σ _α ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	1336 GGCAGTGTGGAGCTGGAGAAGCGCCCCAAGCGCTCTTGGAGCAGCAGCGCGAAAGAGCAG 1395	σ <
AIGCARGACAAGCAGGICGGCITTICCAICCGCAICAGGAGCAGCIAGGTAAGCIGGCACCA) Db (2)	1279 CCAGAGAAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGA 1335 	σ <
NGACTIGANGAGGARGACKATGTICKAGAAGAAGAGGCGAAAGAGGAGGCCAAGCCGGAA	D CY	1219 AGCTCTTCTTCTGTGGATCAGAAGGCTGCCTGAGGAGGAGCAGGAGGAGGAGGAGCAG 1278	σ <
CTGGAGCATGTGCAGCAGGAGGAGCAGGCCCCCGGAAACCCCCACGAGGAGGAC	2 B Q	1159 CCAGAATACATCCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA 1218 	в 4
GASTIAGHANG-AMANGAAGACGCTCAGHAACGATTCAGGAAAGGGACAAGCAATIGG	Db Cy	1099 CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGGTCCTGCCT 1158 	σ <
ANGCASAGGICC I ISSAGGICAGE I SYAGCAGANAGAGGAGAGAGAGAGAGAGAGAAGAAGAAGAAGAAG	ם אל	1039 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC 1098	σ <
	? 5	979 ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT 1038	σ <

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                          GCTTTCAATAGTTTTAAGATTATTTTTAAATGTGTATTTTAGCCTTTTAATAAAAAATCTC
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SH3D1A

CDNA.

SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; th therapy;

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                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4030; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3D1A gene megakaryocytic fineage. The SH3D1A gene megakaryocytic lineage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of CDNA clone (see AAZ34570-74) suggests the streams of softens exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia,
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                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene food supplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #20567.
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, Oligomers, and for chromosome CC polynucleotides are also used in dispostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC disgnostice, forensics, gene mapping, identification of mutations CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ARS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC at ftp.wipo.int/pub/published_pct_sequences.
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GADARCAGGGAGTTTAGGADADARACCTGADATTG-CCCAGGTTATTGCTTCCTACGCTG) B &	2382 TCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCACCCTGGTCTACCACAGAGAAAAGG 2441	B 8
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GIGATIGIGGITACCAAGAAGATGGIGACIGGIGACGGAAGC-GGIGGGCGACAGGC	} B &	2263 CCACGCCCCGGAAAACCCCACGAGGAGACAGACTGAAGAGGGAAAGACAGTGTCAGGAAG 2322	₽ <i>Q</i>
CCAITIFACACHIACGACAGITCIGAGCAAGGAGATTFAACCTTT-CAGCCAGGGGATTFACCTTTTCAGCCAGGGGATCCAGGGGATTTAACCTTTTCAGCCAGGGGATCAGGGGATTTAACCTTTTCAGCCAGGGGGATCAGGGGATTTAACCTTTTCAGCCAGGGGGATTTAACCTTTTCAGCCAGGGGGATTTAACCTTTTCAGCCAGGGGGAT) B &	2206 AGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAGGAGCAG 2262	B 8
CTAMASHAGITACCTTCCCGGCGCCAAGCCACCATTCCCGGAGAA-GAGITTATTG	\$ B \$	2146 AAGCAGAAAGAGCCAGGAGAGAGAAGAGCCTGGAGTTAGAGAAGCGAAAAGGAAGACGCTCAG 2205 	B 8
TCAGGGCCCGTAAGGAAATCCACAAGCAT-CGATACTGGCCCTAATGAAAGTCCTGCTAG) B &	2086 AGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCAGCGGCGACTG 2145	B 8
	B &	2026 AGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGAACTG 2085 	용 성
AACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGG	y dg	1966 GCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGAGGTGGAG 2025	유 성
2966 GTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTATCCTTGGAGAGCC-AAAAAAAGAC 3024 	B &	1907 AGTTAAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCAAAAG-A 1965 	용 성
906 GATCAGCCTTTACCCCAGCCACAGCCACTGGCCACTCCCCTCCCCATCTCCCGTCCTGGCCAGG 91	5 B &	1850 AGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACC 1906 	B 8
891	B &	1794 GAACAAGTCTAGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGC 1849	B 8
) B	1734 AGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCCAGAGGCAAGAAATTGAGAGCAC 1793 	\$ &

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08-N 08-N 08-N 08-N 17-N 17-N	39-A0G-2000; 2000US-022824. 01-SEP-2000; 2000US-0229287. 01-SEP-2000; 2000US-0229343.
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02-00	- TAN- 2000 - 2000II
29-SI	17-JAN-2001; 2001WO-US01309.
29-SI	02-806-2001.
29-SI	
29-SI	WO200155308-A2.
27-SI	nomo adpienta.
27-51	
25-SI	disorder; neurological disease; infection; human;
PR 25-SI	iparasitic; cardiant; gene therapy; cancer; immune disor
PR 21-SI	antiinflammatory: antiulcer: vulnerary: anticonvulsant: antibacterial
14-SI	lmological; cytostatic; immunosuppressive; noot
cide; PR 14-SI	oprotective; nootropic; neuroprotective; antibacterial;
PR 14-SI	Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
14-SI	Human polynucieoride SEQ ID NO 33.
14-SI	
14-SI	22-OCT-2001 (first entry)
14-SE	
12-81	DATE 2925.
18-80	AAI63825 standard; cDNA; 3466 BP.
1S-80	AAI63825
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18-80	3971 ATCTCTTGGATATGTTGACCCCAACTGAAAGAAAGCGACAAGGATACATC 4020
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                  Sequence 3466 BP; 1056 A; 829 C; 861 G; 710 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 33; 664pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acids treating and/or preventing
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                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the ted specification, but was obtained in electronic format dir WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                        CCCCCGGAAACCCCACGAGGAGGACAGACTGAAGAGGGGAAGACAGTGTCAGGAAGAAGGA
                                                                                                                                                            AGTTCAGGAAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAG---
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ABK43498 standard; cDNA; 3319

ВP

05-JUN-2002 (first entry)

encoding novel central nervous system protein #78.

RESULT 10
ABK43498
ID ABK43
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AC ABK43
XX
DT 05-JI
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DY Cent
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KW hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; leukaemia; neovascularisation; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss. 17-JAN-2001; 2001WO-US01332 02-AUG-2001 Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;

31-JAN-2000; 2000US-0179065

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02-OCT-2000

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20-OCT-2000

20-OCT-2000

08-NOV-2000

17-NOV-2000

17-NO
New isolated nucleic acid encoding a preventing, treating or ameliorating food additives or preservatives -
                                                             WPI; 2001-581633/65.
P-PSDB; AAU87168.
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2000US-0186628.
2000US-0186536.
2000US-0186350.
2000US-0189874.
2000US-0198123.
2000US-0215135.
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2000US-0216847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. corneal infection, gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include
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                                                              CAGTGCCAATGGGATCCATTCCAGTTGTTGGAATGTCTCCAACCCTAGTATCTTCTGTTC
                                                                                    CTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCC
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0; Mismatches 412;
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Pred. No. 0;
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                              GCCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGCTAAGAATTGCTGAAAATCACCCACT 1834
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1832; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       clones. 830 cDNA molecules encoding a human protein have been solated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length
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na T, Nagai
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                                               TGCCTGAGGAGCCGTCGTCAGAGGATGAGGAGCAGC---CAGAGAAGAAACTGCCTGTGA 1300
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                             TACCAGAGGAACCAGTTTTAGAAGATGAACAACAACAATTAGAAAAGAAATTACCTGTAA
                                                                                             GAAGAGTTCGATCTGGCAGTGGTATATCTGTCATAAGCTCAACATCTGTAGGTCAGAGGC
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AAZ34573 standard; CDNA; ₽₽

01-FEB-2000 (first entry)

Human SH3D1A cDNA clone

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RESULT 12
AAZ34573
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KW megak
KW plate SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia;

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                                                                                                                                                                                                                                                                                                                                        involving the megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelete on chromosome 21. Sequencing of 5 different sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, methods or chromosome 21. low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress or megakaryocytic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder using a nucleic acid that expresses SH3DIA or its antisense nucleic acid.
                                                                                                                                                                                                                           Query Match
Best Local Sim:
Matches 1783;
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The present invention describes primer sets for synthesising 5602 (full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the CC coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in CC the 5'-end sequence'3'-end sequence is selected from those defined in CC the 5'-end sequence'3'-end sequence is selected from those defined in CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow-obtaining of the full-length CC CNAS seasily without any specialised methods. AAH03165 to AAH13628 and CC AAH13631 to AAH13627 appresent human amino acid sequences; and AAH13629 to AAH13632 to AAH13632 to AAH13633 to AAH13635 to AAH13633 to AAH13635 to AAH13633 to AAH13636 to AAH13639 to AAH1369 to AAH1369 to AAH1369 to AAH1369 to
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Best Local Similarity
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02-MAY-2000;
09-JUN-2000;
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27-AUG-1999;
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Sugiyama
                                                                                                                                                                    GGGATGGTGTGCGCGGCTGCGGACTCGGCGTTCCTCGC-GCGGCGTGCGGGCTGCACTGA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2131 BP; 691 A; 448 C; 572 G; 420 T; 0 other;
                                                                                                                                                                                                                                                                                                                     GAGAAGAGTGGAGGCGCCAGGGGAGGGAGCGTAGCTTGGTTGCTCCGTAGTACGGCGGCT
ACGTAATAGAACCATGGCTCAGTTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGC 305
                                                                                                                                                                                                                                 CGCGAGGAAGAATCCCGAGCGGGCTCCGGGACG
                                                                                                 TTTGTGTGAGGGGGGGGCGCGCGCACCCGGCCGGAGATGAGGCGTCGATCAGCAAGGTGA
                                                                                                                                                <u> GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCTCCCAGCGGCGCGTGAGCGGCACTGA</u>
                                                          TTTGTCCCTGGGGCGGCAGCGCGGACCCGGCGGGAGATGAGGCGTCGATTAGCAAGGTAA
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; 2000JP-0183767.
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99JP-0300253
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T, Wakamatsu
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A, Nagai I
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C, Otsuki
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        GAACTICGAGCGAGGCAGTGTGGAGCCTGGAGAAGCGCCCGCCAAGCGCTCTTGGAGCAGCA
                                                                                                         GATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGGCGGCGTCGTCAGA
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                                                                                           TATATOTOTOATAAGOTOAACATOTOTAGATOAGAGGCTACCAGAGGAACCAGTTTTAGA
                                                                                                                                           ACCTGTCCTGCCTCCAGAATACATTCCACCTTCTTTAGAAGAGTTCGATCTGGCAGTGG
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             ACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAG
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                                                                SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; th
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Cc Sequencing of 5 different sizes of cDNA clone from foetal brain cc (see AAZ34570-74) suggests that at least 3 isoforms exist. The cinvention provides methods for the diagnosis and treatment of invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet clistorder on chromosome 21, low platelets in deletion for cplatelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain cmalformations and corresponding cognitive dysfunctions, complete the suppressing cells unable to regulate themselves; creening for a somatic alteration in the SHDIA gene; monitoring the progress and adequacy of a treatment; monitoring tunour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, chaematopoietic disorder, platelet disorder or leukaemia; and councied to subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a councied of a councied councied
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Matches 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9) corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3231 BP;
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4161 TTTGGGGCTTTCCTAGTCACTCAGACTGAC-CGGCCCGCCTTCACACGGGGCGCTTTCAA 4219	g Q
1963GTCCT 1967	Db
1963 1962 4101 CTGAGTCACTGCGTGCAGAGGCAGAAGCAAATTGCAGAACTGCACAGGGTGGTGGGTCCT 4160	8 8
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3981 ATGGGAGATGCAGCCTTGATCATGTGACTTGCAGCATGATCACCTACTGCCTTCTGAGTA 4040	Ş
3921 CCCTCAGGCTTGAAAGTCCTCAAAGAGACCCACTATCCCATATCACTGCCCAGAGGGATG 3980	₽ Q
3861 TGTAAAGCTGACCACAGACATGGACCCCAGCCAGCAATGAATG	B &
828	DЬ
3801 GGACCCGGACTGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTA 3860	8
3741 CCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGACGTCCTCAACAAGGA 3800	8 8
3681 ACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGACTACACCGC 3740	유 왕
3621 TCCAGGAATTAIGTCAAACTTCTAAGCCCGGAACAAGCAAAATCACCCCAACTGAGCT 3680 	B &
588 AGGTGGATGGTGGGAAGGAGAGCTGCAAGCACGTGGGAAAAAAGCGCCAGATAGGCTGGTT 16	g
3561 AGGTGGATGGTGGGAAGGAGAACTGCAAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTT 3620	8
3501 TGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAGAACCC 3560	B 8
1493GAPATTGCCCAGGTTATTGCCTCATACACCGCCAC 1527	Db .
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3381 AGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGGAA 3440	8
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381 CATTTCAGGGCCCATAAGGAAGTCTACAAGCATGGATTCTGGTTCTTCAGAGAGTCCTGC 1	}
3141 CATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTGC 3200	S.
1321 GTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACT 1380	뫄

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5038 -CCTTAGATATTAGTTGGAAGTCGGGAAGAGAATT 5071	99 GAAATGGAGCTCATGGTCCGTTTGTGTGTT-AGATATGCTGTAGCTGAAGCCCTGTTTGT 2	2741 ATTAATTT-CCAATGTTTACATTTTTTAACTAGACTGT-GGAATTTCTACAGATTAATAT 2798 4980 GAAATGGCGCTCCTGGTCCGTGTGTGTGTGTTAACTTGTGCTGTAGCTGAAGCCGTGTGT 5037	920 ATTAATTTCCCAGTGTTTACATTTTTTAACTAGACTGTGGGGGGTTGCTACAGATTAÀTAT 49	2681 TGACCTATTTTGAACAAGTAATTTTCTTGACAAGAAAGAA	4865TATCTTGAACAAGTAATCTTCTTGACAAGAAAGAATGTATAGAAGTCTCCCTGCA 4919	621: TCCACAGTCTCTTTTAGTCTCTGTTACATGAAGTTTTATTCCAGTTACTTTTCATGGAA 268	4811 CCCACCGTCTTAGTCTCTGTTACGTGAAG-TTTATTCCAGTTGCTTTTTATGGAA 4864	2562 GTGTTTGCATAGCATAAAATCAGTAGACAAC-ACCACTGAGGTCGTTACGATCAACGATA 2620	4751 ATGTCTTCACACCATAAACTAGTAAGACGCCAACTGCCCAGGCGGTTACGATCATCAGTA 4810	2502 TTGTTCGGTCTCAGATTTATCTGGTTGAGTTGGTGTTTTTGTTTTGGGGGTTTTTAATTTTGC 2561	4691 CCGTTTGGTCTCAGATGTACCTAGTTGTGCCCCGTGTTTTTGTTTTTTTT	2442 TGCATTTAATTTTATTTTGCACAGTGACCTTGTAGCCACATGAGAAAGCACTCTGTGTTT 2501	4634GCATTCATTTTACTTTGCACAGTGACCTTGTAGCCACCTGAGGAAGCAC-CCATGTTT.4690	2382 CATAAGAAATTAGTTCTTTCCATGGCAAAGCTATTACCTTGTACGATGCTCTAATCATAT 2441	4575 AAGAAGTAGCT-CTTCCTCCATGGCTAAACCCACCGTGTACAGTGCTCCTCTACT 4633	2322 GTGTTTGTGTTTTGTGTGTGTATCAGCTGTACCTTGTTGAGCATGTAATACATCCTGTA 2381	4516 GGGGTTATGCTTGTGTGACCATCACGTGTACC-TGTCGCGCATGTACCATCTGTACCG 4574	2263 CAGAGGAGTTCAGTATCTCTGTTTTAAAGACGTATA-GAATGAGCCCAATTAAAGCGAAG 2321	4456 CAGAGGAGATGGGTGTACCTGTTTTGAAAATGTGTATGTA	2203 TGTCCAGTGTTACCAACTAAATTGTGCAGTTTGGGGCTTTTCCCCCCTTACCATAGAAGTG 2262	4400 TGTCCAGTGTTCCCAACCACATTGTGTAGTTTGGGGCTGTTCCCTGCCGTAGAGCA 4455	2143 GTGCTATTAAAAATTGTTCCAAATGTCCATAAATCTGAGACTTGATGTATTTTTTCATTT 2202	4340 ACGATTAAAATGCTGTTCCGGGCGTACCGTAAACTGAGAGCTTGCTGTACCCTTTGCCGTT 4399	2088 GACTTCTTTGCTATTTTGGTTTTTGCAAAAAGACCCACTATCAAGGAATGCTGCAT 2142	4280 ACTTCTTTGCCTATTTTGGTTTTTACAAAAACACCCACTATCAAGGAGTGCCTGTCTGCGG 4339	2028 TAGTTTTAAAATTATTTTTAAATATATATTTTAGCTTTTTAATAACAAAATAAAT	4220 TAGTTTTAAAATTATTTTTAAATGTGTATTTTAGCCTTTTAATAAAAATCTCAATCAA

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RESULT 15
AAS84762 standard; cDNA; 2874 BP.
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AC AAS84762;
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DNA encoding novel human diagnostic protein #20566.

Human; chromosome mapping; gene mapping; gene therapy; forensic;

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                                                                                                                                                                                                                                                                                                                                                                                                      CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical considers involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity. CC disposities, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations and CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences.
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Best Local S
Matches 1778
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                         GTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGC
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RESULT 1 BC020269 LOCUS REMARK COMMENT SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2126) BC020269 BC020269.1 Strausberg,R Homo sapiens Homo sapiens, clone IMAGE: 4899011, mRNA Homo sapiens (human) GI:17939664 2126 bp mRNA linear HTC 19-DEC-2001

ALIGNMENTS

Result No.

Score

Match Length DB

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Description

SUMMARIES

Query

1598.2 1582 809.8 804.2

31.4 31.1 15.9 15.8

2126 2079 818 906

BC020269 BC013578 CA324450 BU519029

BC020269 Homo sapi BC013578 Homo sapi CA324450 UI-M-FY0-BU519029 AGENCOURT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIMI at: http://image.llnl.gov Series: IRAL Plate: 40 Row: n Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796 This clone has the following problem: no cloning site / microdeletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                        CCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCA
                                                                                                      CAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATTGCTAGCATGCCA
                                                                                                                                                                        ATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCTGTCATGAAACAG
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/mol_type="mRNA"
/do_xref="taxon:9606"
/clone="nYMAGE:4899011"
/tissue_type="Pancreas, ep/clone=lib="NIH MGC 42"
/lab_host="BH10B_R"-
/note="Vector: poTB7"
/note="Vector: 90TB7"
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Homo sapiens, S
IMAGE:3878242,
                                                                      Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.Series: IRAK Plate: 14 Row: C Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 450
This clone has the following problem: retained intron.
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NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technolog
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Sequencing by: Sequencing Group at the Stanford Human
ter, Stanford University School of Medicine, Stanford,
site: http://www-shgc.stanford.edu
tact: (Dickson, Mark) mcd@paxil.stanford.edu
tact., Schmutz, J., Grimwood, J., Rodriquez, A., and
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                                                                  cgapbs-r@mail.nih.
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National Institutes of Health, Mammalian
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Contact: Robert Strausberg,
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Plate: LLMM14095 row: o column: 18
High quality sequence stop: 701.
Location/Qualifiers
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Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                            GCAAGTTGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGACATGGACCCCAGCCA
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:6516809"
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/note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
Not1; Cloned_unidirectionally. Primer: Oligo dT. Average
insert_size_1.7 kb. Constructed_by_ResGen, Invitrogen
Corp. Note: this is a NIH_MGC Library."
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Query Match Best Local Similarity 98.0%; Pred. No. 1.5e-163; Matches 890; Conservative 0; Mismatches 9; Indels 9; Gaps 8; 936 GCAGTTATTCAACAGCCACGACAAACTATGAGTGGACACTTAACAGGTCCCCAGGCAAG 995	/clone lib=NIH MGC 129" /clone lib=NIH MGC 129" /notee="Organ: olfactory epithelium; Vector: /notee="Organ: olfactory epithelium; Vector: /notee="Organ: olfactory epithelium; Vector: pcMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library." BASE COUNT 271 a 210 c 280 g 150 t	High quality sequence start: 10 High quality sequence stop: 564. FEATURES Location/Qualifiers source /organism="Mus musculus" /mol_type="musA" /db_xref="taxon:10000" /clone="IMAGE:6314690" /lab hose-resistant)"	in the second of	aryota; Metazoa; Chordata malia; Eutheria; Rodentia (bases 1 to 911) -MGC http://mgc.nci.nih.g ional Institutes of Healt ublished tact: Robert Strausberg, il: cgapbs-r@mail.nih.gov	911 bp mRNA linear 1764676 NIH_MGC_129 Mus musculus cDNA clon 1901:22358186 18 (house mouse)	Qy 4190 CCGGCCCGCCTTCACACGGGCG 4212	Qy 4074 GACCTTAGTTGCATGTGATCGAAATGTCTGAGTCACTGCGTGCAGAGGCAGAAGCAAATT 4133	Qy 4014 GCATGATCACCTACTGCCTTCTGAGTAGAAGAACTCACTGCAGAGCAGTTTACCTCATTT 4073
DEFINITION Mus musculus 0 day neonate Cerebellum CDNA, KIKEN TULI-length enriched library, clone:C230068L04 product:intersectin (SH3 domain protein 1A), full insert sequence. ACCESSION AK082606 AK082606.1 G1:26349812 VERSION HTC; CAP trapper. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus. REFERENCE 1 AUTHORS Carninci, P. and Hayashizaki, Y.	828 ACCCACTT 1835 900 ACCCACTT 907 AK082606 2589 bp mRNA linear	1713 780 1772 840	Qy 1596 TGAATGGGAAC-GGAACCGGAGAACTCCTGAATCAGAGGAACAAGAAGACAAGGAGC 1654	Qy 1476 GGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	Db 360 TGTGACATTGAAGATAAAAGCGGGAGAACTTCGAGCGAGC	QY 1236 TCAGAGGCTGCCTGAGGAGGCCGTCGTCAGAGGATGAGCAGCCAGC	OY 1116 TGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCTCCAGAATACATCCCTCC 1175	OY 1056 TGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAAT 1115

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Submitted (1.2)

Physical and Chemical Research (2.2)

Exploration Research Group, RIKEN Genomic Scientific (2.2)

Exploration --- Tearitute; 1-7-22 Suehiro-cho,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2589)
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                                                        Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P.,
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                                                                                                                                                                                              Direct Submission
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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Please visit our web site for further details.
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AGTTTAGGAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCTACTGGTCCC
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HELIVTEENYVNDLOLUTEIFQKPLTESELLTEKEVANIFVNWKELIMCNIKLLKALR
VRKKMSGEKMPVKMIGDILSAQLPHMQPYIRFCSQQLMGAALIQQKTDEAPDFKEFVK
RLANDPRCKGMPLSSFILKPMGRVTKYPLIIKNILMTPSHNHDHSHLKHALEKAEEL
CSQVNEGVREKENSDRLEWIQAHVQCEGLSEQLVFNSVTNCLGPRKFLISGKLYKAKS
NKELYGFLFNDFLLLTQITKPLGSSGTDKVFSPKSNLQYKMYKTPIFLNEVLVKLPTD
PSGDEPIFHISHIDRYYTLAASINERTAWVQKIKAASELYIFTEKKKEEKAYLVRSQ
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Towa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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UI-M-FY0-cde-p-10-0-UI.r1 NIH BMA
IMAGE: 6832091 5', mRNA sequence.
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CA750495.1 GI:25575732
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/mol type="mRNA"
/strain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE: 6832091"
/tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FY0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: Ec.
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AGCTGGAGCGGC

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AAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCCGAGCAGGAGAGGAAAAGAGCGGGAGC

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AAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGC 1147
                                                                                                                                                                      CTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAG 1087
                                                                                                                                                                                                                                                                                                            GTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCCAGG 1027
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AAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGCCACCCGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACACA. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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IMAGE: 5719103 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project Course.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH108 (T1 phage resistant)"
/clone_lib="NIH_BMAP_EXO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed_according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1 % agarose
                                                                                                                                                                                                                                                                                                                                                                                                             (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

151 c 221 g 102 t 1 others
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/db_xref="taxon:10090"
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                                                                                                         Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                        1 (bases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                             Unpublished
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/organism="Mus musculus"
                                  ocation/Qualifiers
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/tlissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DHIOB (TI phage resistant)"
/clone_lib="NIH_BWAP_EHOp"
/clone_lib="NIHBPWAP_EHOP"
/clone_lib="NIH_BWAP_EHOP"
/clone_lib="NIH_BWAP_EHOP"
/clone_lib="NIH_BWAP_EHOP"
/clone_lib="NIH_BWAP_EHOP"
/clone_li
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Pred. No. 1.3
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1.3e-147;
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2568 CCAGACTGGAGAGCCAGGATGGCTTGGAGGAGAGCTGAAAGGGAAGACGGGATGGTTCCC 2627

Query Match Best Local S Matches 734

Similarity

14.2%;

Score 721.2; DB Pred. No. 3e-147; Mismatches

Conservative

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Indels

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Gaps

Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri 1 (Dases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM944544 738.bp mRNA linear EST 14-MAR-20
UI-M-EHOp-bvr-j-08-0-UI.rl NIH_BMAP_EHOp Mus musculus cDNA clone
IMAGE:5695975 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                       198
                 /tissue type="whole brain"
//dev stage="wembryo 18.5 dpc"
/lab_host="PHIOB (TI phage resistant)"
/clone_lib="NIH_BMAP_EHOD"
/clone_lib="NIH_BMAP_EHOD"
/note="Grgan: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Grgan: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Grgan: brain; Vector: pYX-Asc; Site_1: BcoR I;
/note="Grgan: brain; Vector: pYX-Asc; Site_1: BcoR I;
/note="Grgan: brain; Vector: pXY-Asc; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6"
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VERSION
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CB521237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim.Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following repetitive elements were found in this cDNA sequence: 220-337, >(GGA)n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB521237
CB521237.1 GI:29354592
EST.
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UI-M-GHO-cem-g-10-0-UI.rl NIH_BMAP_GHO Mus
IMAGE: 6841475 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 706)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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/ Glain="C3/DH/O
/ Glore="IMAGE: 6841475"
/ Clone="IMAGE: 6841475"
/ tissue_type="whole brain"
/ dev etage="1, 5, and 15 days newborn"
/ dev etage="1, 5, and 15 days newborn"
/ lab_host="DH10B (T1 phage resistant)"
/ clone lib="WIH_BMAP GH0"
/ clone lib-"WIH_BMAP GH0"
/ clone lib-"WIH_BMAP GH0"
/ clone lib-"WIH_GLORE
/ clone lib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                           IMAGE: 6849689 5', mRNA
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UI-M-FY0-cfh-m-16-0-UI.rl NIH_BMAP_FY0 |
IMAGE: 6849689 5', mRNA sequence.
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Mammalia; Eutheria;
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   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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EST.
Mus musculus (house mouse)
Mus musculus
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BU704308
                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 729)
                                                                                                                                                                                   Unpublished
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This clone was contributed by the Brain Molecular Anatomic contributed b
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/dev_stage="embryo 12.5dpc"
/lab_host=="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FOO"
/clone_lib="NIH_BMAP_FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence_located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
76 a 206 c 174 g 172 t 1 others
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/strain="C57BL/6"
/db_xref="taxon:10090"
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Pred. No. 1.2e-143;
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: pYX-5
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TTCCATCCGCATCAGGAGCCAGCCTAAGCTGGCCACCCAGGCACCCTGGTCTACCACAGAG 2436
                                                                                                                                                 GAGCAGCCACGCCCCGGAAACCCCCACGAGGAGGACAGACTGAAGAGGGGAAGACAGTGTC
                                                                                                                                                                                GAGCAGCCACGCCCCCGGAAACCCCCACGAGGAGGACAGACTGAAGAGGGGAAGACAGTGTC
                                                                                                                                                                                                                                                 GACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAG
                                                                                                                                                                                                                                                                                                GACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAG 2256
                                                                                                                                                                                                                                                                                                                                                                                                 GCGCGACTGAAGCAGAAAGAGCAGGAGAGGAAGAGCCTGGAGTTAGAGAAGCAAAAGGAA 2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCA 2136
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                                              AGGAAGAAGGAGGCGGAAGAGAGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTT
                                                                                                                                                                                                                                                                                                                                                  GCGCGACTGAAGCAGAAAGAGCAGGAGAGGAGAGCCTGGAGTTAGAGAAGCAAAAGGAA
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                                                                                                AGGAAGAAGGAGGCGGAAGAGAGAGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTT
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//lab_host="NH10B (T1 phage resistant)"
//clone_lib="NII_BMAP_FY0"
//note="forgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the NotI site and the polyA tail
is AGCGAGACAC. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

28 a 154 c 225 g 94 t 2 others
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/tissue_type="whole brain"
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/strain="C57BL/6"
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Pred. No. 1.8e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 713)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA329050
CA329050.1
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           /clone="IMAGE: 6827736"
/tlissue_type="whole brain"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone=lib="NIH_BMAP_RYO"
/clone=lib="NIH_BMAP_RYO"
/note="COTGAN: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Nat and then cloned
with EcoR I adaptor, digested with Size fraction, ligated
with EcoR I adaptor, digested with Nat and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Towa Rrain Anatomy Project (MAND): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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Brain Anatomy Project (BMAP): 'Gene Discovery in the
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 782) .
NIH-MGC http://mgc.nci.nih.gov/.
                                                                         BG922629
BG922629.1 GI:14303105
                                                                                                       602821583F1 NCI_CGAP_Mam6
                                          Mus musculus
                                                                 EST
                                                                                             mRNA sequence.
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Similarity 98.6%;
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                                                                                                                                                                                                                               GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAAACT
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                                                     mouse)
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Pred. No. 1.1e-140;
0; Mismatches 9;
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s musculus
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Query Match
Best Local Similarity
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Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technolog
cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10905 row: e column: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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TCACTGCGTGCAGAGGCAGAAGCAAATTGCAGAACTGCACAGGGTGGTGGGTCCTTTTGG 4165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGA 3745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATTATGTCAAACTTCTAAGCCCCGGAACAAGCAAAATCACCCCAACTGAGCTACCCA
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                                                                          ACTCACTGCAGAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAG 4105
                                                                                                                                                                                                                                                                             AGGCTTGAAAGTCCTCAAAGAGACCCACTATCCCATATCACTGCCCAGAGGGATGATGGG 3985
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                                                ACTCACTGCAGAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAG
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/tissue_type="infiltrating ductal carcinoma"
/dev_grage="5 months"
/lab_host="DHIOB"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal_Site_2: Not1; Cloned unidirectionally. Primer: Oligo d Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
a 187 c 191 g 180 t
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/strain="FVB/N"
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re greater than or equal to the score of the result being printed,
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6. /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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             GenCore version 5.1.6 (c) 1993 - 2003 Compugen
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US-09-215-681-5
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SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien
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US-09-404-879A-72
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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                                                         CAGGGCCAACAGCTGCCTGGTAGTCCTCCTATCATGAAACAACCCCCTATGTTCTCT
                                                                                                  CAAGGATATCAGCTCCCCTCCACACTTCCCCCCTGTCATGAAACAGCAACCAGTG---GCT
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US-09-620-925-1
US-07-884-811-15
US-07-885-971-15
US-08-194-0888-15
US-08-194-0888-15
US-08-194-0888-15
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PCT-US93-04648-15
US-08-781-891-208
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                                                                 AGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAGAGACAACGCCGTTTA
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Sequence 72, Application US/09338933
Patent No. 648831
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEO ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
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US-09-215-681-72
; Sequence 72, Application US/09215681A
Patent NO. 6528253;
GENERAL INFORMATION:
; APPLICANT: Miccham, Jennifer L.
APPLICANT: King, Gordon B.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OF OVARIAN CANCER FILE REFERENCE: 210121-463;
CURRENT APPLICATION UNMBER: US/09/215,681A;
CURRENT FILING DATE: 1998-12-17;
NUMBER OF SEQ ID NOS: 310
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien

DIAGNOSIS

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Pred. No. 4.3e-116;
0; Mismatches 812;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
PEFFERRICE/DOCKET NUMBER: 1101-174
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GENERAL INFORMATION:
APPLICANT: SPARKS
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TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
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LENGTH: 2873 bases
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DEDNESS: single
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                                                                                                                                                                                              GTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTGGAGAAGTTCAAGGTC 3100
                                                                                                                                                                                                                                                                                                                                                                              CTTTTTCAAACCTAACTCTAAATACATCATGGCAGAAAAAATCAGCCTTCACTCGAACTG
                                                                   ATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTTGGGGAAGGTGCATGGAG
                                                                                                                                                                                                                                         AAGCACAGGCCCTTTGTTCCTGGACTGCAAAGAAAAGATAACCACTTGAACTTCTCAAAAC
                                                                                                                                                                                                                                                                         CTTCTCTGACCGTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCA 2926
                                                                                                     GAAGAGGATGGTTTCCCAAATCTTATGTCAAGATCATTCCTGGGAGTGAAGTAAAACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : (212) 790-9090
(212) 869-8864/9741
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                                   US/08/630,915A
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Pred. No. 1.7e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 2873;
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US-08-630-915A-39
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                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: SPARKS
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APPLICANT:
APPLICANT:
                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                   STREET: 1155 A
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                   COUNTRY: USA
ZIP: 10036-2711
                                                                                                       STATE:
                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
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                                                                                                                                   1155 Avenue of the Americas
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VENTION: POLYPEPTIDES HAVING A FUNCTIONAL VENTION: DOMAIN OF INTEREST AND METHODS OF
                                                                                                                                                                                                                                                                     HOFFMAN, NO. 630
KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                           SPARKS, Andrew B.
PC-DOS/MS-DOS
                                                                                                                                                                                                     USING SAME
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Best Local Similarity 63.9%;
Matches 418; Conservative
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NAME: Misrock, S. Leslie
REGISTRATION UNUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 747 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                             GTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAAGTCAGTGGGCAAGTTGGGCTC
                                                                                                                                                   TATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCTCCAAGGGACAACTCATTAAT
                                                                                                                                                                             TACGATTACACCGCCCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAAC
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TTTCCTTCAAACTACGTTAAGATGACGACAGACTCAGATCCAAGTCAACAGTGA
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Pred. No. 3e-57;
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US-09-404-879A-5 RESULT 6

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; Sequence 5, Application US/09404879A
; Patent NO. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
APPLICANT: Algate, Paul A.
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.463C2
CURRENT EPILICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
INUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapien
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 531
TYPE: DNA
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US-09-338-933-5
; Sequence 5, Application US/09338933
; Patent No. 6488931
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 GATGGAAGGATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 GATAACCTCAAACCTTCAGGAGGTTACATAACAGGTGATCAAGCCCGTACTTTTTTCCTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCCTGTGCC 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGATATCAGCTCCCCCCCACACTTCCCCCCTGTCATGAAACAGCAACCAGTGGCTATT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTTAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAAC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGGCCAAATATGTGGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCCACAGCGATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCAT
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Pred. No. 1.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                 FOR THERAPY
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645

362 585 308 525 248

422

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CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapien
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US-09-215-681-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09215681A Patent No. 6528253
GENERAL INFORMATION:
                                                                                                                                                     Query Match
Best Local Similarity
Matches 264; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 264;
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
                                                                                                                  226 GGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACCCTTTCGGT
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                                                  286 GGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTC 345
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                   GGAGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCAT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCCATTGCC 433
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                                                                                                                                                  Score 151.4; DB 4;
Pred. No. 1.5e-29;
0; Mismatches 161;
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Pred. No. 1.5e-29;
0; Mismatches 161;
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                                                                                                                                                   Indels
                                                                                                                                                                                 Length 531;
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SEQ ID NO 60
LENGTH: 480
TYPE: DNA
ORGANISM: Homo s
US-09-404-879A-60
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US-09-404-879A-60
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Ming, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: DIRANOSIS OF OVARIAN CANCER
TITLE OF INVENTION: DIRANOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
                                                                                                                                                                                                                                                                                                                                                                                                                      Local
 314
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                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
247; Conserv
                                                                                                                                                                                                                       GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 438
                                                                                                                                                                                                                                                                 GAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTTACATAACA 133
                                                                                                                                                                                                                                                                                                                                                                  ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG
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                               GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 618
                                                                                             GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 558
                                                                                                                                                              GGTGATCAAGCCCGTACTTTTTTCCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAA 193
                                                                                                                                                                                                                                                                                                GAPAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 378
                                                                                                                                                                                                                                                                                                                                 ATGGCTCAGTTTCCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAA
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llarity 62.1%;
Conservative
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Pred. No. 1.2e-27;
D; Mismatches 145
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RESULT 10
US-09-338-933-60
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CURRENT FILING DATE: 199-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
                                                                                                                                                            Sequence 60, Appli
Patent No. 652825
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                                                                                                                                              GENERAL INFORMATION:
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                                                            APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: OVARIAN CANCER FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/215,681A CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 310
                                                  FILE REFERENCE: 210121.463
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No. 648893)
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Pred. No. 1.2e-27;
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RESULT 12
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; ORGANISM: Homo
US-09-215-681-60
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Best Local Similarity
Matches 247; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08728323A Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Pattrick S.
TITLE OF INVENTION: Immediate Ea
TITLE OF INVENTION: Sarcoma-Asso
TITLE OF INVENTION: Encoding Sam
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                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
               ATTORNEY/AGENT INFORMATION: NAME: White, John P.
                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                       STATE:
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REGISTRATION NUMBER:
                                                 CLASSIFICATION: 435
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Pred. No. 1.2e-27;
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                                                                                                                  Version
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; NAME/KEY:
; LOCATION:
US-08-728-323A-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Kieff, Blliott D.

APPLICANT: Kallestas, Mary E.

APPLICANT: Kaye, Kenneth M.

TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A U
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME
FILS REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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; TYPE: DNA
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GGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCA
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US-09-410-399-1

US-09-410-399-1

Sequence 1, Application US/09410399

Patent No. 6482597

GENERAL INFORMATION:

APPLICANT: Robertson, Erle S.

APPLICANT: Cotter, Murray A.

TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding

TITLE OF INVENTION: to Genomic Host DNA

FILE REFERENCE: UM-03778
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Pred. No. 4e-27;
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Patent No. 5849564

Patent No. 5849564

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Rdelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM THE PROPERTY ON POLYPEPTIDES FROM TITLE OF INVENTION: HERPESVIRUS, DN
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US-08-770-379-20/c
                                                                                                                                    US-08-770-379-20
                                                       Query Match
Best Local Similarity
Matches 534; Conserv
                                                                                                                                                                                  TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
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                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 278-0400
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CITY: New York
STATE: New Yor
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Title: Perfect score:

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Run on:

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Post-processing: Minimum Match 0%
Maximum Match 10

Listing first 45 summaries

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Description

SUMMARIES

.0 US-09-884-441-72
1 US-09-907-969-72
2 US-09-827-271-72
4 US-10-198-053-72
1 US-09-764-881-55
US-09-879-957-193

Query Match

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0 US-09-764-868-125 US-09-918-995-31258 US-09-879-957-39 US-09-864-761-17127 US-09-864-761-26948 US-09-864-761-17146 US-09-864-761-17146 US-09-864-761-17644 US-09-864-761-333

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

2201672 seqs, 1661799599 residues

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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Sequence 125, Appl
Sequence 193, App
Sequence 195, Appl
Sequence 31258, App
Sequence 31278, App
Sequence 31727, A
Sequence 30453, A
Sequence 30454, A
Sequence 17146, A
Sequence 10314, A
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US-09-884-441-72

Sequence 72, Application US/09884441

Patent No. US20020119158A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C7

CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

LENGTH: 2017
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Sequence 19759, A
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Sequence 17643, A
Sequence 17763, A
Sequence 83, App
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US-09-907-969-72
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Publication No. US20030091580A1
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Algate, Paul A.
APPLICANT: Paing, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Hill, Paul
APPLICANT: Hill, Paul
APPLICANT: Hill, Paul
APPLICANT: AND DIGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
CURRENT FILLING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FASTSEQ for Windows Version 4.0

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; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Homo s
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RESULT 3
US-09-827-271-72
Sequence 72, Application US/09827271
Sequence 72, Application US/09827271
Publication No. US20030165504A1
GENERAL INFORMATION:
APPLICANT: Fanger, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
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Matches 1128; Conservative
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ORGANISM: Homo sapien
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapiens
US-10-198-053-72
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Db 15 GGGCCGCACGCCGCCCGCCCGGAGATTAGCAAGGTAAAAGTAACAGA 74 Qy 256 ACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTG 315 &	Similarity 86.2%; Pred. No. 2.9e-106; 0; Conservative 0; Mismatches 73; Indels GGGCGGCCGCGCACCCGCCCGGAATGAGGCGTCGATCAGCAAGG	Match 8.0%; Score 406	LOCATION: OTHER INFO	; LOCATION: (556) ; OTHER INFORMATION: n equals a,t,g, or c ; NAME/KEY: SITE	OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE	2	; FEATURE: ; NAME/KEY: SITE ; LOCATION: (481)	; LENGIH: 508 ; TYPE: DNA ; ORGANISM: Homo sapiens	PatentIn Vei 55	Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192	APPLICATION NU	APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies	; Publication No. US20030125246A9 ; GENERAL INFORMATION:	RESULT 5 US-09-764-881-55 Commence SS Prolination HC/00764001		QY 2137 GCGCGACTGAAGCAGAAAAGAGCAGGAGAGGAAGAGCCTGGAGTTAGAGAAGAGCAAAA 2192	Db 1902 AAGGAACTCAGAGAAAGCTATAATACACAGCAGTTAGCCCTTGAACAACTTCATAAAATC 1961	QY 2077 AAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGGTCCCTGGAGGCA 2136	Qy 2017 GAGGTGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTG 2076	Qy 1957 CTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGAC 2016	1722 TTANACGANAGANTTANANACATGCAGCTCAGTNACACCTGATTCAGGGATCAGTTTA 178	1897 CTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTCTTACC 1	Qy 1837 CAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAGAAGACTTATTCCAGAGAAACAGATA 1896	QY 1777 CAAGAAATTGAGAGCAACAAGTCTAGAGAGCTAAGAATTGCTGAAATCACCCACTTA 1836	Db. 1542 AAACATCAGCAGATCTCAGGCAGACTACAAGATGTCCAAATCAGAAAGCAAAACACAAAAG 1601
; AINCRE!/AGENT INFORMATION;; NAME: MISTOCK, S. Leslie; REGISTRATION NUMBER: 18,872; REFERENCE/DOCKET NUMBER: 1101-174	CLASSIFICATION IOR APPLICATION I APPLICATION I FILING DATE:	; CUKERT AFFLICATION UNDER: US/09/879,957 ; APPLICATION NUMBER: US/09/879,957 ; FILING DATE: 13-Jun-2001	j j	COMPUTER READABLE FORM: ; COMPUTER FLORDY disk COMPUTER. TRM BC COMPANIAN	USA)36-27	55 Avenue of the 1	; NUMBER OF SEQUENCES: 227 ; CORRESPONDENCE ADDRESS: : ADDRESSER Pennie & Edmonds LLD	THE OF INVEN	FOWLKES, Dana M. MCCONNELL, Stephen J.	HOFFMAN, N. US20020034755Alh KAY, Brian K.		US-09-879-957-193 Sequence 193, Application US/09879957	RESULT 6	Db 552 TANANOGGGTNCCCCTG 568	Qy 735 TAACGGGGCTCCTCCCG 751	Qy 676 GTT-GGAANGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGC 734	Db 433 ATCGCCAGCAACCGCTTACAGCTGTTGCTCCAGTGCCAATGGGGNCCATTCCAGTT 492	Qy 616 ATTGCTAGCATGCCACACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTT 675	Qy 556 CCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGG 615	Qy 496 ATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCC 555	253 CAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTCC	436 CAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGAT	Qy 376 ACTGGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCA 435	Qy 316 GAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAAGCCTGAAGCCGGATAGCGGGATTTATT 375	Db 75 ACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTA 134

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Matches 633;
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 bases
TYPE: nucleic acid
STRANDEDNESS: single
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 GTCCAAGTAGTGAAAGAGCCACACCTGCCTTTCATC--
                              AAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAA
                                                                                                                              CTGGGCAGCTGATTCTGATCCGGAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAACTGC
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                                                                AGGCCAGAGGAAAAAGCGACAGAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTGG
                                                                                                                                                                                             AGATTGCTCAGGTAACTTCAGCATATGTTGCTTCTGGTTCTGAACAACTTAGCCTTGCAC
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Pred. No. 1.1e-84;
0; Mismatches 363;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 4210
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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Best Local :
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                      AGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCCGTAAGGAAATCCA
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                                                                                                 CCGCCAAGCCATTCCCCGGAGAAGAGTTTATTGCCATGTACACATACGAGAGTTCTG
                                                                                                                                                                                                                  GAAGAGGATGGTTTCCCCAAATCTTATGTCAAGATCATTCCTGGGAGTGAAGTAAAACGGG
                                                                                                                                                                                                                                                                                       ATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTTGGGGAAGGTGCATGGAG 1154
                                                                                                                                                                                                                                                                                                                                                           AAGCACAGGCCCTTTGTTCCTGGACTGCAAAGAAAGATAACCACTTGAACTTCTCAAAAC 1094
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AACCTGGAGATTTGACTTTCACAGAAGGTGAAGAAATATTGGTGACCCAGAAAGATGGAG
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ilarity 61.0%;
Conservative
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Pred. No. 4.9e-84;
0; Mismatches 361;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-918-995-31258
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                                                                                                                                                                                                                                    SEQ ID NO 31258
LENGTH: 503
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31258, Application US/09918995 Publication No. US20030073623A1
                                                                                        Query Match
Best Local Similarity
                                                                         Matches
                                                                                                                                                 09-918-995-31258
                                                                                                                                                            FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(503)

OTHER INFORMATION: n = A,T,C or
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   AATTCAGAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATGTCTGGCCAACCA
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                                                                       Score 322.6; | Pred. No. 3.7e
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US-09-879-957-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 39, Applicati
Patent No. US200200347
GENERAL INFORMATION:
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOWALN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-999
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ADDRESSEE: Pennie &
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                                                                                                                                                                                                                                                FILING DATE: 13-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGAGAACTTTGAACGTGGCAACCTGGAACTGGAGAAACGAAGGCAAGCTCTCCTGGAA
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                                                        TELEFAX: (212) 869-8864/9741
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXOI

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MIC

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
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US-09-864-761-17127
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Best Local Sim:
Matches 418;
                                                                                                                                                                                                                 Sequence 17127, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 2.4e-63;
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OTHER INF
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SEQ ID NO 17127
LENGTH: 270
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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FIER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.2

FHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

FIER INFORMATION: EXPRESSED IN PLACENYRA, SIGNAL = 2.3

FIER INFORMATION: EXPRESSED IN PLACENYRA, SIGNAL = 2.3

FIER INFORMATION: EXPRESSED IN PLACENYRA, SIGNAL = 1.6

FIER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

FIER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

FIER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

FIER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

FIER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2

FIER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

FIER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

FIER INFORMATION: SET HUMAN HIT: Q15811, EVALUE 1.00e-112

FIER INFORMATION: NT HIT: g111526214, EVALUE 0.00e+00
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FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00668
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00666
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AAACCAGTGACCGATCTGACATCTGCCCCCTGCCCCCAAACTGGCTCTGCGTGAGACCCCT
                                                                                          GGATGGTTCCCTGCAAACTATGCAGAAAAAGATTCCAGAAAAATGAGGTTCCCACTCCAGCC
                                                                                                                                                                                     GTGGATGAAAGCCAGACTGGAGAGCCAGGATGGCTTGGAGGAGAGCTGAAAGGGAAGACG
                                                                                                                                                        GTGGATGAAAGCCAAACTGGAGAACCCGGCTGGCTTGGAGGAGAATTAAAAGGAAAAGACA
                                                               GGGTGGTTCCCTGCAAACTATGCAGAGAAAATCCCCAGAAAATGAGGTTCCCGCTCCAGTG
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Pred. No. 1.6e-46;
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                  LENGTH: 286
TYPE: DNA
                                                                                                                                               ORGANISM: Homo
                                                                                                                                 FEATURE:
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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   INFORMATION:
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Chen, Wensheng
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Rank, David R
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N: MAP TO APO00311.1

N: EXPRESSED IN BT474, SIGNAL = 0.87

N: EXPRESSED IN HOME MARROW, SIGNAL = 1.3

N: EXPRESSED IN HBL100, SIGNAL = 1.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66

N: EXPRESSED IN LUNG, SIGNAL = 0.66

N: EXPRESSED IN BRAIN, SIGNAL = 0.69
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                  PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
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Best Local Similarity
                                                          PRIOR PRIOR PRIOR
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CURRENT FILING DATE: 2001-05-23
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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FILING DATE: APPLICATION
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el, David K.
NUMBER:
                 2001-01-30
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EXPRESSED IN HELA, SIGNAL = 0.92
EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
NT HIT: AF114488 1, EVALUE 0.00e+00
SWISSPROT HIT: Q15811, EVALUE 2.00e-45
EST_HUMAN HIT: AA773263.1, EVALUE 1.00e-112
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PCT/US01/00662
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Pred. No. 1.7e-46;
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FOR

APPLICATION NUMBER: PCT/US01/00661

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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17146, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                    APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT TETLING DATE: 2001-05-23
DDYOD NOBIT TETLING DATE: 2001-05-23
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Best Local Similarity
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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ORGANISM: Homo sapiens
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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N: EXPRESSED IN HELA, SIGNAL = 2.4

N: EXPRESSED IN HELA, SIGNAL = 1.2

N: EXPRESSED IN PLACENTA, SIGNAL = 0.76

N: EXPRESSED IN HBL100, SIGNAL = 1.3

N: EXPRESSED IN HBL100, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95

N: NT HIT: AF114487.1, EVALUE 0.00e+00

N: EST HUMAN HIT: AA773263.1, EVALUE 1.00e-112

N: SWISSPROT HIT: Q15811, EVALUE 2.00e-45
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Pred. No. 1.7e-46;
0; Mismatches 32;
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LENGTH: 301
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Best Local Similarity
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ORGANISM: Homo
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
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INFORMATION:
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APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
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GCCGCCAAGCGCTCTTGGAGCAGCAGCGCGAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGC
                             GGGCGGAGCAGGAGGAAGGAGCGTGAGCGCCAGGAGCAAGAGCGCAAAAAGACAACTGG
                                                                                         GAAGGCAAGCTCTCCTGGAACAGCAGCGCGCAAGGAGCAGCAGCGCCCTGGCCCAGCTGGAGC
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EXPRESSED IN HETAL LIVER, SIGNAL = 2.6

: EXPRESSED IN BRAIN, SIGNAL = 2.6

: EXPRESSED IN BT474, SIGNAL = 2.3

!: EXPRESSED IN BT474, SIGNAL = 2.2

!! EXPRESSED IN BT474, SIGNAL = 3.4

N: EXPRESSED IN HELA, SIGNAL = 3.7

N: EXPRESSED IN HELA, SIGNAL = 3.7

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2

ON: EXPRESSED IN LUNG, SIGNAL = 2.2

ON: SMISSPROT HIT: 035601, EVALUE 3.50e-01

ON: NT HIT: AF114487.1, EVALUE 1.00e-122

THUMAN HIT: BE542917.1, EVALUE 4.00e-62
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Pred. No. 2e-46;
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FEATURE:
OTHER INFORMATION: EXPRESSEI
OTHER INFORMATION: EXPRESSE
OTHER INFORMATION: EXPRESSE
                                                                                                                                                                                                                      SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 17644
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TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: GENE EXPRESSION ANAL
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                      ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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FILING DATE: 2000-05-26
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00666
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 N: MAP TO AP000049.1
N: EXPRESSED IN BONE MARROW, SIGNAL
N: EXPRESSED IN BULT LIVER, SIGNAL
N: EXPRESSED IN BRAIN, SIGNAL = 4
N: EXPRESSED IN PLACENTA, SIGNAL = 3
N: EXPRESSED IN BT474, SIGNAL = 2.9
N: EXPRESSED IN HBL100, SIGNAL = 2.9
N: EXPRESSED IN LUNG, SIGNAL = 3.2
                                                                                                                                                                                                                                                                                                                      NUMBER: US 09/608,408
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GGAAAGAAATTGAGAGGCGAGAG 263
                         GGAAGGAGATCGAGAGGCGCGAG 1560
                                                                                      GGGCGGAGCAGGAGGAAGGAAGGAGCGTGAGCGCCAGGAGCAAGAGCGCAAAAAGACAACTGG
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EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

EXPRESSED IN HEART, SIGNAL = 2.9

EST HUMAN HIT: BE542917.1, EVALUE 3.00e-62

SWISSPROT HIT: 035601, EVALUE 2.80e-01

NT HIT: AF114487.1, EVALUE 1.00e-122
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/232,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30 APPLICANT: PRIOR PRIOR PRIOR PRIOR PRIOR APPLICANT: Penn, Sharron TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1 APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00662 Hanzel, David I Chen, Wensheng David R. , David K. <u>ဂ</u>

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PRIOR APPLICATION UNMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10314
LENGTH: 480
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Best Local Similarity 81.6%;
Matches 222; Conservative
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.87

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 32

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN PERAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BADULT LIVER, SIGNAL = 0.92

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
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ORGANISM: Homo sapiens
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FILING DATE: 2001-01-30
                                 2763 GCCCTCCACAACCCCCAACAACTGGGCAGACT 2794
                                                                                                                                 2703 CCCTGCCCCAAACTGGCTCTGCGTGAGACCCCTTGCTTTTGCCAGTGACCTCTTTTGA 2762
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449
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GCCCTCCACGACCCCTAATAACTGGGCCGACT 480
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Search completed: December 5, 2003, 06:15:39 Job time : 1089.45 secs

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Human SH3D1A cDNA
DNA encoding novel
Human SH3D1A cDNA.
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Human breast cell	ABA46803	22	270	5.5	198.8	01
	ACA57579	25	701	5.7	206	**
DNA encoding novel	AAS84759	23	395	5.8	210.8	w
ed ex	AAA44038	21	346	٠	250	~
Human SH3P18 gene.	AAT39796	17	747	7.1	258	_
Human cDNA clone (AAH08146	22	676	7.1	260	0
Human cDNA clone {	AAH03435	22	ω	7.7	281	w
cDNA encoding nove	AAS27090	22	4210	9.1	331.4	w
DNA encoding novel	ABK43586	23	3746	9.1	331.4	7
Human clone 65 gen	AAT39799	17	2873	9.1	332.4	٥١
Human ovarian anti	ABQ55007	24	2067	9.4	340.8	01
DNA encoding novel	ABK43814	23	568	9.8	356	#=
cDNA encoding nove	AAS31621	22	568	9.8	356	w
Human polynucleoti	AAI63919	22	568	9.8	356	ņ
	AAI80000	22	548	9.8	356	_
	AAH15260	22	1329	10.6	387.4	0
Ovarian carcinoma	ABN72656	24	2017	13.1	477.4	Ψ
ovarian car	AAA69762	21	2017	13.1	477.4	w
Human cDNA clone r	AAK93179	22	877	13.3	485.4	7
cDNA 5'-e	AAK91610	22	877	13.3	485.4	٠ı
	ACA57641	25	677	14.1	513.8	01
ncodii	AAS02055	22	4	17.8	648	
Ese2 c	AAZ39011	21	3593	18.3	666.6	w
Ese2L	AAZ39026	21	6014	18.6	677	~
Ese2L cod	AAZ39027	21	4975	18.6	677	
	AAZ39010	21	4625	18.6	677	J
Human polynucleoti	AAK52332	22	6103		713.8	w
Allergic disease e	AAL47247	24	5828	٠	721	w
Human SH3P17 gene.	AAT39795	17	1389	23.6	858	7
	AAK94611	22	1676	30.3	1104.2	U١
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equen	AAH16578	22	2131	٠	1259.2	**
ncodin	AAS84762	23	87	35.5	1291.4	w
•	AAK94139	22	13	. 40.7	1483.8	ı
SH3D1A CDNA	4	20	9	41.0	1495	
ດ	AAI63825	22	3466	56.1	•	J
DNA encoding novel	ABK43498	23	3319	56.1	2043.8	Ψ

ALIGNMENTS

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RESULT 1
AAZ39009
 Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; Er-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
WPI; 2000-052802/04
                                                          27-APR-1998;
05-FEB-1999;
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                  Egan SE,
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                  Wang W, Sengar A;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Bse = EH-domain and SH3-domain regulator of endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); sequences antisense to the (I) spolynucleotide; agents that downregulate expression of Ese genes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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     AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG
                                                      GGGGCTCCTCCCGTCATACAGCCTCTGCCTTTTGCGCATCCTGCAGCCACATGGCCA
                                                                                                                         GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC
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                                   GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA
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                                                                       GCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTT
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1260 1260 1200 1200 1140

1380

W Mouse; murine; Esel; Ese2; endocytosis; vesicular tratticking;	2760
BselL coding sequence.	2701 GGCCAGGGTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTGGAGAGCCCAAA 2760
X X 28-FEB-2000 (first entry)	3 2700
AAZ39025;	QY 2641 CGGCAGAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCCCCATCTCCCGTCCTG 2700 AX
RESULT 2 AAZ39025 LD AAZ39025 standard; cDNA; 5144 BP.	Qy 2581 GACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGCCAGTTA 2640 RE Db 2581 GACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGCCAGTTA 2640 III
3601	2521 AACAACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAACGAGAAAGCCAGAAAACG 2580
y 3601 TATGTAAAGCTGACCACAGACATGGACCCCAGCCAGCAATGA 3642	CACCTICTGAGCCCTCCACE
y 3541 GAGGACCCGGACTGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCAT	2461 GCTCTGCGTGAGACCCCCTGCTCCTTTGCCAGTGACCTCTTCTGAGCCCTCCACAACCCCC 252
3481	Oy 2401 GAGGTTCCCACTCCAGCCAAACCAGTGACCAGTCTGACCATCTGCCCCCCGAAACTG 2460
3421	2400
3421	2281 CCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGGATGGCTTGGAGGA 23
(<u>.</u> .	2340
3301	QY 2221 GTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATCACCATCCAG 2280
D 3241 ACTGGTCCCGAACAACTCACCCTGGCTCCTGGCAGCTGATTCTGATCCGGAAAA V 3301 CCAGGTGGATGGTGGGAAGGAAGTGCAAGCTCGAGGGAAAAAGCGCCAGATAG	61 CCCTGGTCTACCACAGAGAAAGGCCCCGCTTACCATTTCTGCACAGAGAGAG
3241	2101 GACAAGCAGAGACACAAAAAACCCCCATCAGGAGCCCAGCCAAGCCCAGGCA 2160
3181 AAAACAGGAAGTTTAGGAAAAAACCTGAAATTGCCCAGGTTATTGCTTACG b 3181 AAAACAGGAAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTACG	2101 GACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAC
3121	QY 2041 AAGAGGGAAGACAGTGTCAGGAAGAAGAGGGGGGAAAGACCGGAAATGCAA 2100 Db
3061 3121	1981 GAGCATGTGCAGCAGGAGGAGCAGCCCCCCGGAAACCCCCACGAGGAG
3061	1981 GAGCATGTGCAGCAGGAGGAGCAGCCCCCCGGAAACCCCACGAGGAGG
b 3001 ATTGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAAG	o o
2941	Db 1861 CAGAGGTCCCTGGAGGCAGCGACTGAAGCAGAAAGAGCAGGAGAGAGA
2881 2941	1801 GTTTTCAACAACCAGCTGAAGGAACTGAGAAGATACATAGCAAACCAGCAACTCCAGAAG 18
, N	01 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAAGAAG 1860
N	QY 1741 CTCCGGGAGCAGCTGGACGAGGTGGAGAGAGACACCAGGTCAAAGCTGCAGGAGAATTGAT 1800 Db 1741 CTCCGGGAGCAGCTGGACGAGGAGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGAT 1800 Db 1741 CTCCGGGAGCAGCTGGACGAGGAGAGAAGAGACCAGGTCAAAGCTGCAGGAGATTGAT 1800 Db Db Db Db Db Db Db
2761 2821	1681 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAG 17
9 2761 AAAGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGC	CCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGT GACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGC

용 성	B &	B 8	B 8	유왕	A 5	유 양	β δ	B 8	용 성	B 8	B 8	당 성	유 정	음 성
3601 3601	3541 3541		3421 3421	3361 3361	3301 3301	3241 3241	3181 3181	3121 3121	3061 3061	3001	2941 2941	2881 2881	2821	2761 2761
601 TATGTAAAGCTGACCACAGACATGGACCCCAGCCAGCAATGA 3642	GAGGACCCGGACTGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAAT 3600	GCCCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAG 3540	CTACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGATTACACC 3480	TTTCCAGCAAATTATGTCAAACTTCTAAGCCCCGGAACAAGCAAAATCACCCCAACTGAG 3420	CCAGGTGGATGGTGGGAAGGAGAACTGCAAGCTCGAGGGAAAAAGCGCCAGATAGGGTGG 3360	ACTGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAGAAC 3300	AAAACAGGGAGTTTAGGAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCT 3240	GGAGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGG 3180	GTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGGAACGGTGGGCGACAAGTCC 3120	ATTGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAAGGGGAT 3060	GCTAGTCTAAAGAGAGTGGCTTCCCCGGCCGCCAAGCCAGCC	CTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCT 2940	ATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	AAAGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAC 2820

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                                                                                                                                                                                                                                                                                                                                                                                     The present invention specifically describes mammalian Esel and 2 CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein) vestcular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polymucleotide; agents that downregulate CC expression of Ese genes or antagonists of an Ese binding partner are CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of CC Esel is used to block clathrin-mediated endocytosis in vivo or in cell CC cultures, while administration of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal CC proliferation of cells that can be stimulated to proliferate by a growth CC cused to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC dynamin to the complex. Generally conditions that can be treated include CC cancer; abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Esell-coding sequence.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3640; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
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     GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT
                                   GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA
                                                                                                                      GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA
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                                                                                                                                               GAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAAGCAGCGGGAGCTGGAGCGG
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3481 GCCCAGAACGATCACCGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAG -	421 C	361	301 0	3241 ACTGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAAGAAC	3181 AAAACAGGGAGTTTAGGAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCT	3121 GGAGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGG	р р	001	2941 GCTAGTCTAAAGAGAGTGCCTTCCCCGGCCGCCAAGCCAGCC	881	2821 ATGTGGTGGTTTGGAGAAGTCAAGGTCAGAGGGTTGGTTCCCCAAGTCTTACGTGAAA	761	701	641	1	1 1	461

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                                                                                   The present invention specifically describes mammalian Esel and 2 CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein), vesicular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polynucleotide; agents that downregulate CC expression of Ese genes or antagonists of an Ese binding partner are CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of CC Esel is used to block clathrin-mediated endocytosis in vivo or in cell CC cultures, while administration of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal CC proliferation of cells that can be stimulated to proliferate by a growth CC factor receptor; and similar compounds (also inactive Ese mutants) can be CC used to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Esell CDNA sequence.
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse, murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH1-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; 88.
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding of endocytosis, used e.g.
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05-FEB-1999;
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CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT
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                                                                                                    AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGGAGCCGTCGTCAGAGGATGAGCAGCAG
                                                                                                                                                                      CCAGAATACATCCCTCCCTTCCGAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA
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     The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                   Egan
                                                                                                                                                                    Claim
                                                                                                                                                                                                                                          New nucleic acid encoding of endocytosis, used e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998;
05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Esel full length cDNA sequence
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vesicular trafficking and
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CC Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I) specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular CC function. Particularly overexpression of Esel is used to block CC clathrin-mediated endocytosis in vivo or in cell cultures, while CC administration of (I) is used to promote endocytosis of selected cells. CC (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of CC cells that can be stimulated to poliferate by a growth factor receptor; CC and similar compounds (also inactive Ese mutants) can be used to prevent CC complex. Generally conditions that can be regulated, in vivo or in cell CC cultures, by forming an Ese-Espl5 complex, then binding dynamin to the CC complex. Generally conditions that can be treated include cancer; CC abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission.
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Sequence 5082 BP; 1363 A; 1253 C; 1391 G; 1075 T; 0 other;

밁 Ş 밁 Ş 문 Ş 밁 δ 밁 S 뭕 S 밁 Ś 밁 Ś 밁 S 밁 Ś 멍 5 밁 S Matches 3641; Query Match Local Similarity 919 661 859 601 541 739 481 679 421 619 361 559 301 499 241 439 181 379 121 319 259 721 799 61 μ GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCCGATAGCGGGATTTATTACT ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 60 ACAGGTCCCCAGGCAAGAACTAFTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC 480 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA **AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG** GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA GGAATGI GCTAGCATGCCACCACACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT Conservative 99.7%; <u>.</u> Score 3630; Pred. No. 0; Mismatches 멂 21; o ;: Indels Length 5082; ۳ Gaps 378 318 720 660 858 600 540 420 618 360 300 498 240 438 978 918 798 738 678

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CC involving the megakaryocytic lineage. The SH3DIA gene maps to the command candidate region for low platelets on chromosome 21.

Sequencing of 5 different sizes of cDNA clone from foetal brain CC (see ARZ34570-74) suggests that at least 3 isoforms exist. The CC invention provides methods for the diagnosis and treatment of CC megakaryocytic abnormality, myeloproliferative disorder, platelet disorder on chromosome 21. low platelets in deletion for CC platelet disorder on chromosome 21. low platelets in deletion for CC platelet disorder on chromosome 21 with leukaemias, neural CC platelet disorder on chromosome 21 with leukaemias, neural CC platelet in deletion for CC platelet constitue and corresponding cognitive dysfunctions, comic cocphaly, lissencephaly, and colpocephaly. Methods are also CC provided for: suppressing cells unable to regulate themselves; CC screening for a somatic alteration in the SH3DIA gene; monitoring CC the progress and adequacy of a treatment; monitoring tunour risk CC progress or megakaryoctyic abnormality, myeloproliferative disorder, comegakaryoctyic abnormality, myeloproliferative disorder, comegakaryoctic abnormality, myeloproliferative disorder, comegakaryoctic abnormality myeloproliferative disorder, comegakaryoctic abnormality myeloproliferative disorder, comegakaryocytic abnormality myeloproliferative disorder.
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Sequence
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Matches Query Match Best Local Similarity 3167; 479 241 419 181 121 299 239 359 61 μ. GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180 GAAAGGGCCAAGCATTACAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG GAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATCTGGATTCATTACT ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG ATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATA GGTGATCAAGCTAGAAACTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAG GCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTCTGCACTTCCCCCT Conservative 78.4**%;** 86.8**%;** 0, Score 2856; Pred. No. 0; Mismatches 475; DB 20; Indels Length 5195; 9 Gaps 240 300 478 358 298 60 538 418 120

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GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT

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2035 AGACTGAAGAGGAAGACACTGTCAGGAAGAAGGAGGAGGAGAGAGA	B &		961 AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGGAGCCGTCGTCAGAGGATGAGCAGCAG 1020
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859 -	da V		541 AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG 600
799 A) B &		481 GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTTGCGCATCCTGCAGCCACATGGCCA 540
739 1	, B &		421 GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC 480
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CC involving the megakaryocytic lineage. The SHIDIA gene maps to the CC small candidate region for low platelets on chromosome 21.

CS sequencing of 5 different sizes of cDNA clone from foetal brain CC (see AR234570-74) suggests that at least 3 isoforms exist. The CC invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet CC disorder, acute leukaemia, neural disorders, thromobocytopenia, CC platelet disorder on chromosome 21, low platelets in deletion for CC 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain CC malformations and corresponding cognitive dysfunctions, CC microcephaly, lissencephaly, and colpocephaly. Methods are also CC provided for: suppressing cells unable to regulate themselves; CC recening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, CC haematopoietic disorder, platelet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a control of the contr
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ACATCCCT	TGCACCTA	GGAATCTT GGAATCTT	CCCAGGCA	TGAAATAC	CATTCGAT	CTTCCTTC	CTCCCGTC.	CTCCACCC	TGCCACCA	AACAGCAA AACAGCAA	AGCTTATC	CGCTAGCG	AAGCGAGG AAGCTAGA	CCAAGCAT	AGTTTCCC	77.7%; Similarity 86.5%; 7; Conservative	t expres; 1671 A
CCTTCCTTCCTTCCTTCCCTTCCCTTCTTTTTTTTTTT	ATTGATGTT	TCTGACATI	AGAACTATT	AGGCAGTTI AGGCAATTI	GTCGCCAGO GTGGCCAGO	AGCAGATCI AGTAGATCI	ATACAGCCT	TTAGTATCI	CTCACAGCT	CCAGTGGCT	AAACTGAAC AAACTGAAC	GACATGAAI GACATGAAI	AACTTTTTT AACTTTTTT	GACCAGCAO GATCAGCAO	ACACCTTTO	7%; Scon 5%; Prec 0; N	вев SH3D1 ; 1201 С;
AGAAGAGT AGAAGAGT CTGCCTGA	GCCATGTC	GATCAAGA	CTCATGCA	ATTCAACAG	GCCCCTCC GTCCCACC	GGTCCAGG	CTGCCTGC	TCTGTCCC	GTTGCTCC	PATTTCCAG	CTACAAGG	PAACGATGG	TTCCAATC	STTCCTTAG	GGTGGTAG	Score 2831; DE Pred. No. 0; O; Mismatches	expresses SH3D1A or its 1671 A; 1201 C; 1307 G;
TCGCTCCGC	TGGTCAGCC	TGGAAAACT GGAAAACT	ATCAAGTTT GTCAAGTTT	CCACGACAA TCATGACAA	AGCAGCAGA AGTGGCAGA	GTCACAATT GTCACAACT	GTTTGCGC! ATTTGCTC!	TCCAGCAGO	TGTGCCAAT	TGCACCAGO	ATATCAGCI ATATCAGCI	aaggatigg <i>f</i> aagaatigg <i>f</i>	TGGGTTACC	CCTGAAGCC	CCTGGATGI	DB 20; s 475;	acid that expresses SH3D1A or its antisense nucleic e 5458 BP; 1671 A; 1201 C; 1307 G; 1279 T; 0 other;
CAGTGGGA CAGTGGTA CGTCAGAGG	ACTGCCGC	CACTGCAG	ACCCCAGG	AACTATGAG AACTATGAG	ATGGGCTG	AAACACTAI	TCCTGCAG	AGTGCCTC	GGGCTCCA	ATTTGGTA:	CCCCTCCAC	TCAAGTGG	TCAGCCTG	GATAGCGG	CTGGGCCA	Length 5	e nucleion o other;
CCAGAATACATCCCTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA	CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT	TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC	ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT	TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA	GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA	AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG	GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTTGCGGATCCTGCAGCCACATGGCCA	GGAATGTCTCCACCCTAGTATCTTCTGTCCCTCCAGGAGGAGTGCCTCCCCTGGCTAAC	GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT	GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT	GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT	ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGAT	GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA	GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGGATAGCGGGATTTATTACT	ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG	458; 21; Gap	e acid.
TA 960 	CT 900 CT 1166	TC 840 	CT 780	TA 720 TA 986	CA 660 CA 926	AG 600 - AG 866	CA 540 CA 806	AC 480 AC 746	TT 420 TT 686	TT 360 TC 626	CT 300	TA 240 TA 506	AA 180 AG 446	CT 120 	AG 60 AG 326	8 3;	
																	
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -

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supplement; medical imaging; diagnostic; genetic disorder;
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC trestore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences of data and products dependent on DNA and CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC at ftp.wipo.int/pub/published_pct_sequences.
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AAZ34570 standard; cDNA; 5199

01-FEB-2000 entry)

Human SH3D1A CDNA.

RESULT 8
AAZ34570
ID AAZ3
XX
AC AAZ3
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DT 01-F
XX
DE Huma
XX
KW SH3D
KW mega SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder:

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                                                                                                                                                                                                                                                                                        at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21; low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3D1A gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryocryic abnormality, myeloproliferative disorder, having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a platelet disorder.
                                                                                                                                                                            Query Match
Best Local Sim
Matches 2960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          platelet disorder; neural disorder; thromobocytopenia;
haematopoietic disorder; cognitive dysfunction; microcephaly;
haematopoietic disorder; cognitive dysfunction; microcephaly;
haematopoietic disorder; cognitive dysfunction; microcephaly;
haematopoietic disorder; holoprosencephaly; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           megakaryocytic lineage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid from the human SH3D1A gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
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                                                                   GAAAGGGCCAAGCATGACCAGCAGCTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT
                                                                                                                              ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCCATAACTGTGGAG
       GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA
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                                       GAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATCTGGATTCATTACT
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208..3642
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                                                                                                                                                                                                                                                                               expresses SH3D1A or its
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CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCAGCTGGAG
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                                                       GAGCGGTTGGCTCAGCTGGAGCGCCGCCGAGCAGGAGAGGAAAGAGCGGGAGCGCCAGGAG
                                                                                                                        GGCAACCTGGAACTGGAGAAACGAAGGCAAGCTCTCCTGGAACAGCAGCGCAAGGAGCAG
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2155 CAGGCACCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGAGAGAGTGTA 2214	2188 CTGGAGCATGTGCAGCAGGAGGACCAGGAACCAAGAAAACTCCACGAAGAAGAGAA 2247 2035 AGACTGAAGAAGACAGTGTCAGGAAGAAGAGAGGCGAAGAGAGAG	ANCIANAGICO	CAGCTCCGGGAGCAGCTGGACGAGGTGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATT 1	1536 ALIGICISMA LOCICIAN LIACACCIAGA LICANGUA CANADA CANAD	38 GAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGG 1	1408 CAAGAGCGCAAAAGAACAACTGGAACTGGAAAGCAACTGGAAAAGCAACGGAGCTAGAA 1467 1258 CGGCAGCGAGAGGAGGAGGAGGAGGAGGAGGAGCTAGAAACGGAAA 1317
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3235 GCTGCTACTCCGAACAACTCACCTCGCCCCTGGGCAGCTGATTCTGATCCGGAAA 3294	115 AAGTCCGGAGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGGCTCTGGAACT 208	3148 AGTCCTGCTAGTCTAAAGCAGTAGCCTCTCCAGCAGCCAAGCCGATCGGTTCGGGAGAA 3207 2995 GAGTTTATTGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAA 3054 3208 3207 3055 GGGGATGTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGAACGGTGGGCGAC 3114 3208	2815 CAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	848 CAGTTAAGGCAGAGGTCCGCCTTTACTCCAGGCCACGGCCACTGGCTCCTCCCCGTCTCCCGGCCACGGCCAGGCCTTAAAGGCAGAGCCCTTCCCCGGAGA 695 GTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTACAAGCCCTGTATCCCTGGAGA 6	2515 ACCCCCAACAACIAGGCTTCAGTTCCACGAGCCCAGGAGCTCAACGAGCACAACACCA 25/4 2718 ACCCCTAATAACTGGGCCGACTTCAGCTCCACGTGGCCCAGCAGCAGCATGAGAACCA 25/4 2728 ACCCCTAATAACTGGGCTTCAGCTCCACCTGGCCCACCAGCACGAATGAGAAACCA 2787 2575 GAAACGGACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTCAACCGTACCTAGTGCTGGC 2634	335 GGAGGAGAGCTGAAAGGGAAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATTCCA

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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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07-JUL-2000;
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2000US-0237037
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The invention describes an isolated nucleic acid molecule (I) encoding a convel central nervous system protein. (I) and polypeptides (III) encoded (I) are used to treat a medical conditions and in diagnosis of a combination. Disorders which are diagnosed or treated include actionismume diseases e.g. rheumatoid arthritis, hyperproliferative (I) disorders e.g. neoplasms of the breast or liver, cardiovascular disorders (I) cardiac arrest, cerebrovascular disorders e.g. cardiovascular disorders (I) angiogenesis, nervous system disorders e.g. Alzheimer's disease and (I) amylotrophic lateral sclerosis, infections caused by bacteria, viruses (I) angiogenesis, nervous system disorders e.g. Alzheimer's disease and (I) administration and infection, gastrointestinal disorders e.g. dysphagia, (I) adenocarcinomas and irritable bowel syndrome, reproductive system (I) adenocarcinomas and irritable bowel syndrome, reproductive system (I) adenocarcinomas and irritable bowel syndrome, reproductive system (I) activated infection, gastrointestinal disorders e.g. disbetes (I) and pituitary dwarfism, cancers and disorders at the cellular level e.g. (I) activated infection. The polypeptides can also be used to aid wound healing and (I) infarction. The polypeptides can also be used to aid wound healing and (I) infarction. The polypeptides can also be used to aid wound healing and (I) infarction organs before transplantation, for supporting cell culture of (I) concrease or decrease storage capabilities, fat content, lipid, protein, (I) increase or decrease storage capabilities, fat content, lipid, protein,
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                                               CCAAGTGCCGGCCAGTTAAGGCAGAGGTCCGCCTTTACTCCAGCCACGGCCACTGGCTCC
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AAI63825 standard; cDNA; 3466

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 33

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RESULT 10
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AC Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; nantificamatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ss. 31-JAN-2000; 2000US-0179065 04-FEB-2000; 2000US-0180628 24-FEB-2000; 2000US-0184664 17-JAN-2001; 2001WO-US01309.

02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000;

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30-JUN-2000; 07-JUL-2000; 07-JUL-2000;

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08-NOV-2000;
08-NOV-2000;
                                                    WPI; 2001-488781/53.
P-PSDB; AAM43519.
                          New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
        Claim 1; SEQ ID NO 33; 664pp + Sequence Listing; English
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3-0229345. 3-0229509. 3-0229513. 3-0230437.

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2000US-0225268

2000US-0224519. 2000US-0225213.

2000US-0224518

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CC The invention relates to human polynucleotides (AAI63803-AAI64012) and CC the encoded proteins (AAM43497-AAM4366) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the CC specification. The nucleic acids, proteins, antibodies and (ant)agonists CC are useful in the diagnosis, treatment and prevention of: (a) cancer, CC e.g. breast and ovarian cancer and other cancers of the adramal gland, CC come, bone marrow, breast, gastrointestinal tract, liver, lung, or CC urogenital; (b) immune disorders e.g. Addison's disease, allergies, CC autoimmune hammolytic anaemia, autoimmune thyroiditis, diabetes mellitus, CC crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infectious diseases such as viral, bacterial, fungal CC core.
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CC involving the megakaryocytic lineage. The SH3DIA gene maps to the CC small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone from footal brain CC (see AAZ34570-74) suggests that at least 3 isoforms exist. The CI invention provides methods for the diagnosis and treatment of CC megakaryocytic abnormality, myeloproliferative disorder, platelet CC disorder, acute leukaemia, neural disorders, thromobocytopenia, myeloproliferative disorder, platelet CC platelet disorder on chromosome 21. low platelets in deletion for CC 21, association of gains in chromosome 21 with leukaemias, neural cabnormalities, dysfunctions and disorders including brain cabnormalities, dysfunctions and disorders including brain conference of suppressing cells unable to regulate themselves; conference of a somatic alteration in the SH3DIA gene; monitoring the progress or megakaryocytic abnormality, myeloproliferative disorder, consequence of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a concleic acid that expresses SH3DIA or its antisense nucleic acid.
Query Match
Best Local S
Matches 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence of a cDNA clone, termed clone 5, corresponding to a novel human SH3 gene, termed the SH3DLA gene, the contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DLA gene maps to the
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GAATTAGAAAAAAAAAAAAAAA
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RESULT 12 AAK94139 ID AAK94 XX AAK94 AC AAK94 XX O6-NC DT O6-NC XX Human XX Human XX Human XX Homo XX EP113 XX EP113 XX O7-JU

AAK94139 standard; cDNA; 2131 ВP

06-NOV-2001 (first entry)

Human full-length cDNA, SEQ ID NO: 2646

Human; full length cDNA; cDNA synthesis; oligo-capping;

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Best Local
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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                             GGGGCTCCTCCCGTCATACAGCCTCTGCCTTTTGCGCATCCTGCCACCACATGGCCA
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                GGGGCTCCCCCTGTTATACAACCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCCA
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences. disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity from WIF

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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
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gene, that contributes to the development of platelets and the SH3DIA corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of luwaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelets on chromosome 21.

Sequencing of 5 different sizes of cDNA clone from footal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring
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haematopoietic disorder, platelet disorder or leukaemia; and
treatment of a subject (including a prenatal subject) having
megakaryocytic abnormality, myeloproliferative disorder,
platelet disorder, leukaemia or neural disorder using a
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                                                                     AGGAGACATAGTCATGGTGGATGAAAGCCAAACTGGAGAACCCGGCTTGGCTTTGGAGGAGA
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                                                                                                                                                                                                                                                                              CAAGCTGGGTCGGCTTTTCCATCAACACCAAGAACCAGCTAAGCCAGCTGTCCAGGCACC
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Pred. No. 3.7e-289;
0; Mismatches 272; Indels 216;
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•	CGC 3482	3423 ACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGACTACACC
)CT 3422 CC 1707	363 TCCAGCAAATTATGTCAAAC
	TT 3362	3303 AGGTGGATGGTGGGAAGGAGAACTGCAAGCTCGAGGGAAAAAAGCGCCAGATAGGGTGGTT
	CC 3302	3243 TGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAGAACCC 330
	AC 3242 	3183 AACAGGGAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCT
	1492	49
	AA 3182	3123 AGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGG
·	1492	49
	GG 3122	90
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	GT 3062	00
	1492	. 4.
	AT 3002	94
	GC 2942	2883 CATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTG
	CT 2882 	2823 GTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTTCCCCCAAGTCTTACGTGAAAC1
	AT 2822 	2763 AGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACAT
	AA 1260	01 CCAGGGTGAAAAGGTGGAGGGCTACAAGCTCAAGCCCTA
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	264 114	583 CAACTGGGATACGTGGGCGGCTCAGCCTTCTGACCGTACCTAATGCTGGCCAACTGGTGGCCAACTGTGGCCAACTGTGGCCAACTGCTGGCCAACTGCTGGCCAACTGCTGGCCAACTGCCGGCCAACTGCCAACTGCCGGCCAACTGCCGAACTGCCGGCCAACTGCCAACTGCCGGCCAACTGCTAACTGCCGGCCAACTGCCGGCCAACTGCCGGCCAACTGCCGGCCAACTGCCGGCCAACTGCCGGCCAACTGCTGACCGGTTCCAACTGCCGGCCAACTGCGGCCAACTGCGGCCAACTGCGGCCAACTGCGGCCAACTGCGGCCAACTGCGGCCAACTGCGGCCAACTGCGGTGCAACTGCGGTGGCAACTGCGGTGAACTGCAACTGAACTGCAACTGAACTGCAACTGAACTGCAACTGAACTGCAACTGAACTAACT
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	AA 2522 AA 1020	ACAACCCCC ACGACCCCT
	GC 2462	2403 GGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCCTGCCCCCAAACTGG

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1888 TGTGAAGCTGACCACAGCATGGACCCAAGCCAATGA 1927	3603 TGTAAAGCTGACCACAGACATGGACCCCAGCCAGCATGA 3642	1828 GGACCCTGACTGGAGAAAGGAGAAAGTCAATGGACAAGTGGGGCTCTTCCCCATCCAATTA 1887	3543 GGACCCGGACTGGTGGAAAGGACAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTA 3602	1768 GCAGAATGACGATGAGCTTGGCCTTCAACAAGGGCCAGATCATCAACGTCCTCAACAAGGA 1827	3483 CCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGAA 3542

Search completed: December 4, 2003, 15:50:26 Job time: 608.079 secs

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Run
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Listing first 45 summaries
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UI-M-GH0-	B5215	CB5215	14	8	8	54.	17
UI-M-EWO-	794	BQ1794	13	9	8	56.	16
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UI-M-FYO-	2445	CB2445	14	8	8	84.	14
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ALIGNMENTS

REMARK COMMENT REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION RESULT 1 BC013578 KEYWORDS DEFINITION Snoo JOURNAL USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
DNA Sequencing by: Sequencing Group at the Stanford, CA 94305 Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Homo sapiens, Similar to intersectin 1 (SH3 domain protein), clone IMAGE:3878242, mRNA.
BC013578
BC013578.1 GI:15488896 Strausberg, R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2079) Homo sapiens BC013578 Direct Submission Homo sapiens (human) 20,79 bp mRNA linear HTC 04-MAR-2003

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Score

Match

Length DB

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Description

1496.6 1495. 809.8 795.6

41.1 41.0 22.2 21.8

2079 2126 818 911

BC013578 BC020269 CA324450 BQ942708

BC013578 Homo sapi BC020269 Homo sapi CA324450 UI-M-FY0-BQ942708 AGENCOURT

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BASE COUNT
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796
This clone has the following problem: retained intron.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
Contact:
Dickson, M
R. M.
                                                      GCACAATCATTCGATGTCGCCAGCGCCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA
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    TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA
                                  GCACAGTCATTTGATGTGGCCAGTGTCCCACCAGTGGCAGAGTGGGCTGTTCCTCAGTCA
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/mol type="maxNA"
/db_xref="taxxon:9606"
/clone="IMAGE:3878242"
/tissue_type="Lung, large cel:
/clone_Tib="NIH MCC 68"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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(Dickson, Mark) mcd@paxil.stanford.edu
1., Schmutz, J., Grimwood, J., Rodriquez,
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86.0%;
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                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LINL at: http://image.lln Series: IRAL Plate: 40 Row: n Column: 1
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 4
This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven Jones, Jennifer Asano, Tan Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
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Homo sapiens, clone IMAGE:4899011,
BC020269
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2126)
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/mol_type="mRNA"
                                                                                              /note="Vector:
                                                                                                            tissue type="Pancreas,
/clone_lib="NIH_MGC_42"
/lab_host="DH10B-R"_
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Mus musculus
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Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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1 (bases 1 to 818)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gen
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Contact: Robert Strausberg,
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The following repetitive elements were
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                                                                                                                                                                                GATGAGCAGCAGCAGAGAAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAAGAAC
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/tlissue_type="whole brain"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="DHIOB (TI phage resistant)"
/clone_lib="NIH_BMAP FYO"
/clone_lib="NI
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/strain="C57BL/6"
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BQ942708
BQ942708.1 GI:22358186
EST.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High quality sequence start: 10
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Location/Qualifiers
 /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6314690"
/lab_host="DH10B (phage-resistant)"
/clone_tib="WIH_MGC_129"
/note="Organ: olfactory epithelium; V
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                                                                                                                           TGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGT-GTCGACTGGCAACCC
                                                                                                                                                                 GCCACCCGTGGTCCTGAAAGCAAGGAGGAAGACTCTGGAGTTTGAGTTACAAGCTCTGAA
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3 210 c 280 g 150 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                           The FANTOM Consortium ar Group Phase I & II Team.
                                                                                                                                                                                                                                                                             Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                     and Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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2890 GGGCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTGCTAGTCTA 2949

Matches Query Match

Best

Local

Similarity

20.6%;

Score 748.8; DB 11; Pred. No. 1.8e-157;

Length

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Icoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagaki, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.
Please visit our web site for further details.
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Division of Experimental Animal Research in Riken contributed to
                                        693
                                                                                                         YTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTGGDKSGVFPSNYVRLKDSEGSGTAGK
TGSLGKKPELAQVLASYAATGPEQLTLAPGQLILITKKNPGGWREGELQARGKKRQIG
WFPANYVKLLSPGTSKITPTELPKTNAVPAVCQVIGMYDYTAQNDDELAPSKGQIINV
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FFIRDLEQSVLCITVEERDQLSADDFLGRTEIRVADIKKDQGSKGPVTKCLLLHEVPT
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
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/db_xref="GI:26349813"
/translation="PHFRGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPGEEFIAM
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protein 1A) (MGD|MGI:1338069, GB|NM_010587, evidence:
BLASTN, 99%, match=2267)
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/clone="C230068L04"
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CA750495.1 GI:25575732
EST.
Mus musculus (house mouse
Mus musculus
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 732)
                                                                                                                                                                                                                                                                                                                  CA750495 732 bp mRNA linear UI-M-FY0-cde-p-10-0-UI.rl NIH_BMAP_FY0 Mus musculus
                                                                                                              Contact: Robert Strausberg,
                                                                                                                                  Unpublished
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Query Match
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This clone was contributed by the Brain Molecular Anatomy
ATGAGCAGCAGCCAGAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAG
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="MINIB (TI phage resistant)"
/clone_lib="NIH_BMAP_FYO"
/clone_lib="NIH_BMAP_FYO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/note="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/note="Organ: Brain; Vector: pYX- Asc onstructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector: The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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/clone="IMAGE: 6832091"
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/strain="C57BL/6"
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CB248849.1
EST.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB248849 725 bp mRN7
UI-M-EXO-byj-m-24-0-UI.rl NIH_BMAP_EXO
IMAGE: 5719103 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BMAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is clone was contributed by the Brain Molecular Anatomy Project
                                                                        /dev_stage="embryo 15.5 dpc"

//lab host="UH108 (TI phage resistant)"

//clone lib="uH1 BMAP EXO"

//clone lib="nH BMAP EXO"

//clone lib="nH BMAP EXO"

//clone lib="nH BMAP EXO"

//note="Organ: brain; Vector: pyx-Asc; Site_1: EcoR I;

//note="Organ: brain; Vector: pyx-Asc; Vector: The library tag

//note="Organ: brain; Vector: pyx-Asc; Vector:
(BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE: 5719103"
/tissue_type="whole brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
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     Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 732)
                                                                                                                                                                                                               UI-M-EH0p-buu-o-05-0-UI.rl NIH_BMAP_EH0p Mus musculus IMAGE:5687260 5', mRNA sequence.
                                                                                Mus musculus (house mouse)
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No. 4.1e-152;
                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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TITLE
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Best Local :
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                               GGATGTGATTGTGGTTACCAAGAAAGATGGTGGTGGACGGGAACGGTGGGCGACAA
TGGGAAAACAGGGAGTTTAGGAAAAAAACCTGAAATTGCCCCAGGTTATTGCTTCCTACGC 3236
                                                                          GTCCGGAGTCTTCCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGC
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/dev stage="embryo 18.5 dpc"
/lab_host="PHIOB (TI phage resistant)"
/clone_lib="NIH_BMAP_EHOD"
/clone_lib="NIH_BMAP_EHOD"
/note="Grgan: brain; Vector: pYX-Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed_according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence_located between the Not I site and the polyA tail
/is CAGCCACAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

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99.3%;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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738 bp mkNA Linear Wiscolns cDNA clone
UI-M-EHOp-bvr-j-08-0-UI.rl NIH BMAP_EHOp Mus musculus cDNA clone
IMAGE:5695975 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                       Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                     primer: pYX-5
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/mol type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
/cloine="IMAGE:5695975"
/tissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="0H108 (T1 phage resistant)"
/cloine_11b="NIH_EMAP_EH0p"
/cloine_11b="NIH_EMAP_EH0p"
/cloine_11b="NIH_EMAP_EH0p"
/site_2: Not I; The library was constructed_according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone was contributed by the Brain Molecular Anatomy Project
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BU704308 729 bp mRNA linear UI-M-FCO-bzs-j-21-0-UI.rl NIH_BMAP_FCO Mus musculus
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99.5%;
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Pred. No. 1.8e-151;
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Best Local Similarity
Matches 719; Conserv
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 729)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE: 6406772 5', mRNA
BU704308
BU704308.1 GI:23632308
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                 GCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTA
                                                                                                                              TCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAGGCACAATCATTCGATGTCGCC 621
                                                                                                                                                                                                           TCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCCGTCATACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole brain"
/dev stage="embryo 12.5dpc"
/lab_host="DH108 (TI phage resistant)"
/clone lib="NIH BMAP FOO"
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/note="Organ: Brain down as size fractionated on a 1% agarose
gel. First strand cDNA was size fractionated on a 1% agarose
gel. First strand cDNA was size fractionated on a 1% agarose
gel. First strand cDNA was size fraction, ligated
gel. First strand cDNA was size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
with EcoR I adaptor, digested with NotI and the polyA tail
is TGAGAGGC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   program coordinator.
a 206 c 174 g
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 704.8; DB 13;
Pred. No. 8.6e-148;
0; Mismatches 3;
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                                                                                                                                                 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                   CB521237 706 bp mRNA
UI-M-GH0-cem-g-10-0-UI.rl NIH BMAP GH0
IMAGE: 6841475 5', mRNA sequence.
CB521237
CB521237.1 GI:29354592
EST.
EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                sequence: 220-337, > (GGA) n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                       Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 706)
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                          The following repetitive elements were found in this cDN/
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6841475"
                                                                                  Location/Qualifiers
                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                       Ph.D.
                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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/tissue_type="minute Disting"
/dev stage="1, 5, and 15 days newborn"
/lab_host="DH108 (TI phage resistant)"
/clone lib="NIH_BMAP GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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Query Match Best Local Similarity 1006 GAGGATGAGCAGCCAGAGAAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAG 1066 AACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCCGCCAAGCGCTCTTGGAGCAGCAG 946 GGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCA ATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGT 1651 CAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAATTGAGAGCACGAACAAGTCT ACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTT CTCCTGAATCAGAGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAAG GCAAAACGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAA GCAAAACGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAA CGGGAGCTGGAGCGGCAGCGAGAGGAGGAGGAGGAGGAGGAGGCGCGAGGCCC CGGGAGCTGGAGCGGCAGCGAGAGGAGGAGGAGGAGGAGGAGGCGCGAGGCCC GAGCGCCAGGAGCAGCGCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG GAGCGCCAGGAGCAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG CGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCCGCCGAGCAGGAGAAGAAGAAGAGCGG CGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCCGGAGCAGGAAGAGAAGAGCGG AACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCCCAAGCGCTCTTGGAGCAGCAG GGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCA AGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAA 1609 CAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAATTGAGAGCACGAACAAGTCT Conservative 19.3%; 99.6%; ٥, Score 701.8; DB Pred. No. 4e-147; Mismatches 14; u -Indels Length 0 Gaps 1545 1485 1425 1365 1185 1125 1065 1005 660 480 420 360 1305 1245 60 600 540 300 240 180 120 0

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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 703)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CB527154.1 GI:29360627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: pYX-5
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                                         AAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCA
                                                                                     GAGGTGGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTG
                                                                                                                                   GAGGTGGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTG
                                                                                                                                                                                                                       CTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGAC
                                                                                                                                                                               CTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGAC
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                      /dev stage="embryo 13.5,14.5,16.5,17.5dpc"
//lab_host="PHH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FYO"
/clone_lib="NIH_BMAP_FYO"
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agazose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the NotI site and the polyA tail
is AGCGAGACAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

228 a 154 c 225 g 94 t 2 others
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/tissue_type="whole brain"
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strain="C57BL/6"
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                                                                                                                                                                                                                                                                                        Score 699.4; DB 14
Pred. No. 1.4e-146;
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H_BMAP_FY0 Mus musculus cDNA clone
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UI-M-FY0-cdc-j-23-0-UI.rl NIH_BMAP_FY0
IMAGE: 6827736 5', mRNA sequence.
                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 713)
NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house
                                                                                         sequence: 341-458, >(GGA)n#Simple_repeat
                                                                                                        The following repetitive elements were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>AGGAAGAAGGAGGCGGAAGAGAGAGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTT</u>
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                                                                      primer: pYX-5
                                                                                                                                             clone was contributed by the
organism="Mus musculus"
/mol_type="mRNA"
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse)
                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Veri
Sciurognathi;
                                                                                                                                               Brain Molecular Anatomy Project
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thi; Muridae; Murinae; Mus
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CDNA clone
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/strain="C57BL/6"

/db_xref="taxon:10090" /clone="IMAGE: 6827736"

cDNA clone EST 12-FEB-2003

713

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ACTCCTGAATCAGAGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAA 1424
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            TCAGGATATCAGGTGTCGACTGGCAACCCCAGAGGCAAGAAATTGAGAGCACGAA 1538
                                                                                                                                GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTC
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH108 (T1 phage resistant)"
/clone_lib="MIH_BMAP_FYO"
/clone_lib="MIH_BMAP_FYO"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonalio, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence_located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
99 a 157 c 245 g 106 t 6 others
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Pred. No. 9.9e-145;
0; Mismatches 9;
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AUTHORS
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                               686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB244555

ORANGE: 6833270 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The following repetitive elements were found in this cDNA sequence: 413-530, >(GGA)n#Simple_repeat Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB244555.1
TGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTC
                                                                                                                                         ATCAAGTTTACCCCAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGA
                                                                                              ATCAAGTTTACCCCAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 688)
                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                             //Libele_Type="winde Drain"
//dev stage="mbryo 13 5,14 5,16.5,17.5dpc"
//lab_host="DH10B (TI phage resistant)"
//clone_lib="NIH_BMAP_FYO"
//clone_lib="NIH_BMAP_FYO"
//note="Corgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the NotI site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

88 a 156 c 235 g 109 t
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/mol_type="mRNA"
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/tissue_type="whole brain"
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Pred. No. 2.7e
0; Mismatches
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BASE COUNT

199

Matches 704; Query Match

Conservative

<u>,</u>

825

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Local Similarity

19.0%; 98.6%;

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RESULT 15
BQ719508
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                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13583 row: c column: 24
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BQ719508.1 GI:21858405
EST.
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IMAGE:6188111 5', mRNA sequence.
BQ719508
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                quality sequence stop: 6
Location/Qualifiers
organism="Homo sapiens"/
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                                                   GTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGA 1010
                                                                                                    CGTCCTGCCTCCAGAATACATCCCTTCCTTCCAGAAGAGTTCGCTCCGGCAGTGGGAT
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                    ATCTGTCATAAGCTCAACATCTGTAGATCAGAGGCTACCAGAGGAAACAGTTTTAGAAGA
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/dev_stage="adult, 16 yr"
/lab_host="PH108"
/clone_lib="Lupaki sympathetic trunk"
/clone_lib="Lupaki sympathetic trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally_cloned using the following adaptors:
5'-TCGACCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGACGGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
Technologies."

94 a 247 c 218 g 217 t 3 others
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/db_xref="taxon:9606"
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Pred. No. 3.1e-137;
0; Mismatches 141;
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Search Job ti	Db	γQ	В	Ş	Db	.8	Db	Ş
Search completed: December 5, 2003, 00:39:55 Job time : 4658.38 secs	900 GACCCCAGAACAGAGCGCAAA 921	1187 АСССССАССАССАССАССАСА 1208	840 GCAAGGAAGCAGAGCGCCCANNCTGAACGGGCCGACCAGGAAAAGAAAGGAACGT 899	1127 GCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAAGAAGAAGAGCGGG 1186	781 ACTTTGAACGTGGCAACCTGGAACTGGAGAAACGAAG-CAAGCTCTCCTGGNAACGCAGC 839	1067 ACTICGAGCGAGGCAGTGTGGAGCTGGAGAAAGCGCCGCCAAGCGTCTTGGAGCAGCAGC 1126	721 TGAACAACAATTAGAAAAGAAATTACCTGTAACGTTTGAAGAATAAGAAGCGGGAGA 780	1011 TGAGCAGCAGCCAGAGAAGAAGCTGCCTGTGACATTTGAAG-ATAAGAAGCGGGAGA 1066

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Title: Perfect score: Sequence:

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          2003, 15:25:00 ; Search time 158.185 Seconds (without alignments)
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANG
FELLE REFERENCE: 20121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILLING DATE: 1999-09-24
JUMBER OF SEQ ID NOS: 393
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
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Best Local Similarity
Matches 1111; Conserv
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US-08-194-088-15
US-08-194-088-15
US-08-781-891-208
US-08-781-891-208
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Pred. No. 1.9e-109;
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AATCAGAGGAACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCCAAGGAGGAGAAGACTCTG
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210.121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
INUMBER OF SEQ ID NOS: 312
SOFTWARE: Fast SEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-72
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US-09-318-933-72
US-09-318-933-72
; Sequence 72, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                   Matches 1111;
GAAAGGGCCAAGCATTATATTACT
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                                                                     GAACGAGGAAACATGGAGCTGGAGAAGCGACGCCAAGTGTTGATGGAGCAGCAGCAGCAGGG
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                                             Sequence 72, Application US/09215681A
PALENT NO. 6538253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO.
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 198-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FASTSEQ for Windows Version 3.0
SEG ID NO 72
TENCENT 211
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US-09-215-681-72
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Best Local S
Matches 631
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GENERAL IN
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: USA
COUNTRY: 10036-2711
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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DEDNESS: single
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                                                         ATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTTGGGGAGGTGCATGGAG 777
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                                                                                       GAAGAGGATGGTTTCCCAAATCTTATGTCAAGATCATTCCTGGGAGTGAAGTAAAACGGG 837
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KAY, Brian K.
FOWLKES, Dana M.
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WENTION: POLYPETTIDES HAVING A FUNCTIONAL
VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
VENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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US-08-630-915A-39
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                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                       APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    CITY: New York
STATE: New York
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                          STREET:
                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                          1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                               SPARKS, Andrew B.
HOFFMAN, No. 6309820h
KAY, Brian K.
FOMIKES, Dana M.
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                                                                                                                                                                              Pennie & Edmonds LLP
PC-DOS/MS-DOS
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Best Local Similarity 63.9%;
Matches 418; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,915A
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MOLECULE TYPE:
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NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) /20 TELEPHONE: (212) 869-8864/9741
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                                  GTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAAGTCAGTGGGCAAGTTGGGCTC
                                                                                                                                          TATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCTCCAAGGGACAACTCATTAAT
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 TTTCCTTCAAACTACGTTAAGATGACGACAGACTCAGATCCAAGTCAACAGTGA 747
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Pred. No. 7.6e-55;
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RESULT 6 US-09-404-879A-60

Query Match

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Score 144;

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; Sequence 60, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILS REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 60
                                                                                                          GENERAL INFORMATION:
APPLICANT: Witcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: OVARIAN
FILE REFERENCE: 210121.462C1
CCURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 60
SEQ ID NO 60
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US-09-338-933-60
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-60
                                      US-09-338-933-60
                                                                                                                                                                                                                                                                                                                            Sequence 60, Application US/09338933 Patent No. 6488931
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                                                    LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT ELIUNG DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 60
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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RESULT 10 US-09-338-933-5

Sequence 5, Application Patent No. 6488931 GENERAL INFORMATION: APPLICANT: Mitcham, Jen

Jennifer Lynn

US/09338933

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; SEQ ID NO 5; LENGTH: 531; TYPE: DNA; ORGANISM: Homo sUS-09-404-879A-5
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Best Local Similarity 62.1%;
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4622C
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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                   GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCC
                                                                                    GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT
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Pred. No. 2e-26;
0; Mismatches 145; Indels
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CURRENT APPLICATION NUMBER: US/09/215,681A;
CURRENT FILLING DATE: 1998-12-17;
NUMBER OF SEQ ID NOS: 310;
SOFTWARE: FRASTSEQ for Windows Version 3.0;
SEQ ID NO 5;
SEQ ID NO 5;
LENGTH: 531;
TYPE: DNA
ORGANISM: Homo sapien
US-09-215-681-5
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US-09-215-681-5
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TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-5
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Best Local Similarity
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                                      Best Local Similarity Matches 247; Conserv
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION UMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
CURRENT FILING DATE: 1999-06-23
CURRENT FILING DATE: 1999-06-23
                                                                                                                                                                                                                                                                                            APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
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Pred. No. 2e-26;
0; Mismatches 145; Indels
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                                                                                                     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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            STRANDEDNESS:
TOPOLOGY: li
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STATE: New York
COUNTRY: U.S.A.
                                             TYPE: nucleic acid
                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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1185 Avenue of the Ame
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Russo, James J.
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Sarcoma-Associated Herpesvirus,
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Best Local Similarity 45.1%;
Matches 534; Conservative
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Pred. No. 5e-26;
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US-09-298-568-1
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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Best Local Similarity
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Patent No. 6322792
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APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: REPAINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REPERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
EARLIER FILING DATE: 1998-11-19
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TYPE: DNA
ORGANISM: Kaposi's
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GGGCACCGTGGTCCTGAAGGCAAGGAAGACTCTGGAGTTTGAGTTAGAAGCTCTGAA 1454
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SEQ ID NO 1
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US-09-410-399-1
                                                                                                                                     APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09410399
Patent No. 6482587
Query Match
Best Local Similarity
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Best Local Similarity 45.1%;
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-08-770-379-20
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                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 522
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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CITY: New York
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Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
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Search completed: December 5, 2003, 00:46:40 Job time : 164.185 secs

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Result
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Listing first 45 summaries
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WPI; 2000-052802/04. N-PSDB; AAZ39008, AAZ39009.	Egan SE, Wang W, Sengar A;	(HSCR-) HSC RES & DEV LP.		27-APR-1998; 98CA-2230201.	27-APR-1999; 99WO-CA00375.	04-NOV-1999.	MO9955/28-AZ.		Мив вр.			endocytosis;	••	Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking;		Mouse Esel protein sequence.	zo-fab-2000 (liibt chtly)	(6:	AAY57444;		AAY57444 standard; Protein; 1214 AA.	LT 1 7444	

New nucleic acid encoding of endocytosis, used e.g. infection -

Page

43;

99pp;

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The present sequence represents mouse Esel. The present invention CC specifically describes mammalian Esel and 2 proteins (I) and their splice CC variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) CC are involved in regulation of clathrin-mediated endocytosis (as a complex CC with Espl5 protein), vesicular trafficking and actin cytoskeleton. CC Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); sequences antisense to the (I) CC polynucleocide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block CC clathrin-mediated endocytosis in vivo or in cell cultures, while CC (Ant)agonists of (I) is used to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent CC viral infection. Endocytosis may also be regulated, in vivo or in cell C cultures, by forming an Ese-Espl5 complex, then binding dynamin to the CC complex. Generally conditions that can be treated include cancer; CC abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission.
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LIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEI
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                                                               ELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGR
                                                                                                                                                 QREEERRKEIERREAAKRELERQRQLLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEF
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                       27-APR-1998;
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                            QREEERRKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFE
                                                                               SVELEKRRQALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQRELER
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                                                                     megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoletic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy.
                                                                                                                                   SH3D1A; human;
                                                                                                                                                                                            01-FEB-2000
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                                                                                                                                  Down's syndrome; leukaemia; cancer;
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conn clone 11 (see AAZ34572). SH3DIA contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The gene maps to the small candidate region for low platelets on chromosome 21. The protein includes SH3 domains and EH domains, both associated with protein protein interactions and the latter with maintenance of the cytoskeleton. At least 3 isoforms of SH3DIA exist (see AAY32154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myelogroliferative disorder, platelet disorder on neural disorders, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, alteration in the SH3DIA gene; monitoring the progress or and adequacy of a treatment; monitoring tumour risk progress or megality abnormality methods are also provided.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Fig 11; 99pp; English
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92.9%; Pred. No. 0;
tive 39; Mismatches
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SH3DlA; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative dis
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                                                                                                                                                                                                                                                                                                                                TATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASY 1078
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                                                                                                                                                                                                                                                                                                                                                                             both associated with protein interactions and the latter with maintenance of the cytoskeleton. At least 3 isoforms of SH3DIA exist (see AN32154-58). The inventions provides methods for the diagnosis and treatment of megakaryocytic abnormality. The diagnosis and treatment of megakaryocytic abnormality myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided: for suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, and haematopoietic disorder, platelet disorder or leukaemia; and
                                                                                                                                                                                                                                                                       Query Match
Best Local Sim
Matches 1129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA clone 21 (see AAZ34571). SH3DIA contributes to the devel of platelets and the pathogenesis of leukaemias, both in gener and in particular those involving the megakaryoytic lineage. gene maps to the small candidate region for low platelets on chromosome 21. The protein includes SH3 domains and EH domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  platelet disorder; neural disorder; thromobocytopenia;
haematopoietic disorder; cognitive dysfunction; microcephaly;
lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy:
                                                                                                                                                                                                                                                                                                                                     Sequence
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                                    KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                               ASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWP
                                                                                                                                                          IWALADMUNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGI
                                                                                                                                        IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSALPPVMKQQPVAISSAPAFGMGGI
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This sequence represents the protein encoded by the novel human SHJDIA gene (see AAZ34570). SHJDIA contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The gene maps to the small candidate region for low platelets on thromosome 21. The protein includes SHJ domains and EH domains, both maintenance of the cytoskeleton. At least 3 isoforms of with maintenance of the cytoskeleton. At least 3 isoforms of SHJDIA exist (see AAY32154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided: for suppressing cells unable to regulate themselves; screening for a somatic alequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, and corresponderic disorder, platelet disorder or leukaemia; and corresponderic disorder, platelet disorder or leukaemia; and
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                                                                                                                                          GGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLPVTSSEPST
                                                                                                                                                                                                                                                                                                          QAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWL
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                    VKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPGEEFIAMYTYESSEQGDLTFQQ
||||||| :||||||| :||
                                                                     VLGQGEKVEGLQAQALYPWRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGQKGWFPKSY
                                                                                       VLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSY
                                                                                                                                                                                                                                                                                     QAPWSTAEKGPLTISAQENVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWL
                                                                                                                                                                                                                                                                                                                                                            LEHVQQEDEHQRPRKLHEEEKLKREESVKKKDGEEKGKQEAQDKLGRLFHQHQEPAKPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPEKQILNDQLKQVQQNSLHRDSLVTLKRALEAKELARQHLRDQLDEVEKETRSKLQEI
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VKLISGPIRKSTSMDSGSSESPASLKRVASPAAKPVVSGE-
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87.2%;
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Pred. No. 0;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food addition for communication; cell proliferation; skin aging;
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2000US-0190076.
2000US-0198123.
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22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
23-AUG-2000;
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2000US-0233623

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2000US-0232401.
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S-0239935.
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system procein. (I) and polypeptides (III) encoded by (II), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. archiverative disorders e.g. system disorders e.g. Alzheimer's disease and amylotrophic lateral scleronis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. ocrneal infection, gastrointestinal disorders e.g. dysphagia, canders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. diabetes e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. mail are e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. mail are e.g. diabetes e.g. diabetes and content and content e.g. mail are e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. mail are e.g. diabetes and content e.g. diabetes e.g. diabetes e.g. diabetes and e.g. diabetes e.g.
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                      leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. monallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding a protein preventing, treating or ameliorating medical food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; SEQ ID No 686; 837pp; English
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                                                                   EPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGS
                                                                                                                     PGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLPVTSS
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92.3%; Pred. No. 3.76
tive 28; Mismatches
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                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AA'63803-AAI64012) and CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The CC genes were isolated from a range of human tissues disclosed in the CC specification. The nucleic acids, proteins, antibodies and (antiagonists CC are useful in the diagnosis, treatment and prevention of: (a) cancer, CC e.g. breast and ovarian cancer and other cancers of the adrenal gland, CC cone, bone marrow, breast, gastrointestinal tract, liver, lung, or CC urogenital; (b) immune disorders e.g. Addison's disease, allergies, CC conh's disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as myocardial ischaemias; CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly CC from WIPO at ftp. wipo.int/pub/published_pct_sequences.
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Best Local S
Matches 838
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01-DEC-2000;
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06-DEC-2000;
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                                                                                                                                                                                                                                                                                                                   Sequence
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                        TGSCLGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLP
                                                                       KSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                       KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                                                                    ASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWP
                                                                                                                                                                      IWALADMINIDGRMDQVEFSIAMKLIKLKLQGYQLPSALPPVMKQQPVAISSAPAFGMGGI
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                                      -GPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLP
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                              (HYSE-) HYSEQ INC.
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Matches 603;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                              DMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPGEE
                                                                                                                             LRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQ
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MAQFFTFFGGSLDVWAITVEERAKHDQQFLSLKFIAGFITGDQARNFFFQSGLPQPVLAQ 60

Matches 656;

Conservative

187;

Mismatches

274;

Gaps

29;

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  Query Match
Best Local Similarity
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Takahashi
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(NIGE-) JAPAN
(EISA) EISAI
                                                                                                                                                                                                                  The present invention relates to a method for examining allergic diseases with intersectin 2 gene or a gene with equivalent function of intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the eosinophils in a patient, and comparing the expression level with that in the eosinophils of a healthy individual. The method is for examining allergic diseases, particularly atopic dermatitis, which is
                                                                                      Sequence
                                                                                                                                                                 for examining allergic diseases, particularly atopic dermatitis, was also applicable in screening candidate compounds for remedies. The present sequence is a human protein described in the exemplificati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for examining allergic diseases by differential display intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients -
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                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 78-86; 90pp; Japanese.
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                                                                                                                                          the invention.
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DB; AAL47247.
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                                                                                   PTESPASLKRVAS--PAAKPAIPGEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWT
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                       This sequence represents the protein encoded by the human SH3DIA CC CNNA clone 5 (see AAZ34573). SH3DIA contributes to the development CC of platelets and the pathogenesis of leukaemias, both in general cand in particular those involving the megakaryocytic lineage. The gene maps to the small candidate region for low platelets on CC chromosome 21. The protein includes SH3 domains and EH domains, CC both associated with protein-protein interactions and the latter CC with maintenance of the cytoskeleton. At least 3 isoforms of CC sH3DIA exist (see AAY32154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, CC myeloproliferative disorder, platelet disorder, acute leukaemia, CC neural disorders, thromobocytopenia, platelet disorder on CC chromosome 21, low platelets in deletion for 21, association of CC gains in chromosome 21 with leukaemias, neural abnormalities, CC dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, maicrocephaly, liseencephaly, CC and colpocephaly. Methods are also provided: for suppressing CC cells unable to regulate themselves; screening for a somatic cells unable to regulate themselves; screening for a somatic cells unable to disorder, platelet disorder or leukaemia; and corresponding characteric disorder, platelet disorder or leukaemia; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Fig 13; 99pp; English.
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                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
            09-AUG-2001
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
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20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hamunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with useful in diagnosis and gene therapy -
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N-PSDB; AAK52332.
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Similarity 51.0%;
56; Conservative 18
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                                                 VDGDGQLKAEEFILAMHLTDMAKAGQPLPLTLPPELVPPSFR-----GGKQI----DSING
                                                                                                  PKTGTSEWAVPQPTRLKYRQKFNTLDKSMSGYLSGFQARNALLQSNLSQTQLATIWTLAD
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                                                                                                                                                   IQPLP-IPYSSSTLPHGSSYSLMMGGFG---GASIQKAQSLIDLGSSSSTSSTASLSGNS
                                                                                                                                                                          IQPLPAFAHPAATWPKSSSFS--RSGPGSQLNTKLQKAQS-FDVASAPP------
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Wang D,
Yang Y,
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2000US-0654936.
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, Zhang J, Ren
n T, Goodrich R;
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Pred. No. 4.1e-188;
7; Mismatches 274;
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 Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking;
                           Mouse Ese2 protein sequence
                                                      28-FEB-2000
                                                                               AAY57445;
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                                                                                                                                                                                                                              KLLGPSSERATPAFHP-
                                                                                                                                                                                                                                          KLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDELAPSKGQIINVLNKEDPDWW 1186
                                                                                                                                                                                                                                                                               KKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHV
                                                                                                                                                                                                                                                                                               KKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYV
                                                                                                                                                                                                                                                                                                                                                                                   GGRGWFPKSYVKIIPGSEVK-----REEPEALYAAVNKKPTSAAYSVGEEYIALYPY
                                                                                                                                                                                                                                                                                                                                                                                                             GQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVAS--PAAKPAIPGEEFIAMYTY 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPTVSLSATS-----TSSEPLSSNQPASVTDYQN-VSFSNLTVNTSWQ--KKSAFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVGEPGWLYGSFQGNFGWFPCNYVEKMPSSENE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKKSLEKEELC-QRLKEQLDALEKETASKLSEMDSFNNQLKCGNMDDSVLQCLLSLLSCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TLKAEEKKRETASVLVNYRALYPFEARNHDEMSFNSGDIIQVDEK
                                                     (first
                                                                                                         Protein;
                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----EKQKRLQEEKTQEKIQEEERKAEEKQRKDKD-------
                                                                                                         1197
                                                                                                                                                                                                                            -VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KAVSPKKAL-----
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with Esp15 protein), vesicular trafficking and actin cytoskeleton. CC Generally (1) (or its (ant)agonists, minerics, fragments and inactive mutants); (1)-specific antibodies (Ab); sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or castociated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Ese1 is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while cambinistration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proinferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to provent cultures, by forming an Ese-Esp15 complex, then binding dynamin to the complex. Generally conditions than to an be treated include cancer; then can cell division or migration; viral infection; or abnormal cell division or migration; or abnormal cell division or migration; or abnormal cell division or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents mouse Ese2. The present invention specifically describes mammalian Ese1 and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding of endocytosis, used e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ39010, AAZ39011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Page 48; 99pp; English
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05-FEB-1999;
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      1197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Esel and 2 proteins, involved in regulation for treating cancer or preventing viral
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Query Match Best Local Similarity Matches 658; Conserv 174 165 120 119 61 61 MAQFFTPFGGSLDVWAITVEERAKHDQQFLSLKFIAGFITGDQARNFFFQSGLPQFVLAQ 60 VIQPLPAFAHPAATWPKSSSFS--RSGPGSQLNTKLQKAQS-FDVASAPP-----GIASMP-----PLTAVAPV--PMG-----SIPVVGMSPPLVSSVPPAAVPPLANGAPP 164 IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG 118 ---SMPNLSIHOPLPPVAPIATPLSSATSGTSIPPLMMPAPLVPSVSTSSLP---NGTAS 173 IWALSDLNKDGKMDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGMG 119 MAQFPTAMNGGPNMWAITSEERTKHDKQFDNLKPSGGYITGDQARTFFLQSGLPAPVLAE LIQPL-SIPYSSSTLPHASSYSLMMGGFG---GASIQKAQSLIDLGSSSSTSSTASLSGN ----AAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLS 26 Conservative 177; 48.6%; Score 3049.5; DB 21 52.4%; Pred. No. 3.9e-187; tive 177; Mismatches 275; 21; Indels 145; Length 1197; Сарв 60 32

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1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPKTGTSEWAVPQPSRLKYRQKFNSLDKGMSGYLSGFQARNALLQSNLSQTQLATIWTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEV
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YTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                             KNTSGWWQGELQARGKKRQKGWFPASHVKLLGPSSERTMPT
                                                                                   KNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYD
                                                                                                                                                                                                                                                                      PASLKRVASPAAKPAIP-GEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGD
                                                                                                                                                                                                                                                                                                               NHLNFSKHDVITVLEQQENWWFGEVHGGRGWFPKSYVKLIPGNEVQRGEPEALYAAVTKK
                                                                                                                                                                                                                                                                                                                                         NHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISG-PVRKS--TSIDTGPTES
                                                                                                                                                                                                                                                                                                                                                                                                  --TW-----QQKSAFTRTVSPG-SVSPIHGQGQAVENLKAQALCSWTAKKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVY
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                                                                                                                                           RTGIFPSNYVRPKDQENFGNASKSGASNKKPEIAQVTSAYAASGTEQLSLAPGQLILILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KALSPKKALLPPTVSLSATSTS-SQPPASVTDYHNV--SFSNLTVNT--
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                                                          ----FHAVCQVIAMYD
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RESULT 13 AAY57450

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standard; Protein; 1658

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61 IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG

118 119

60 60

IWALSDLNKDGKMDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGMG

GIASMP-----PLTAVAPV--PMG-----SIPVVGMSPPLVSSVPPAAVPPLANGAPP 164

---SMPNLSTHQPLPPVAPIATPLSSATSGTSIPPLMMPAPLVPSVSTSSLP---

-NGTAS

1 MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ

MAQFPTAMNGGPNMWAITSEERTKHDKQFDNLKPSGGYITGDQARTFFLQSGLPAPVLAE

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Query Match Best Local Sim Matches 658;

Similarity

48.6%; 177;

Score 3049.5; DB 2 Pred. No. 6.1e-187; '7; Mismatches 275;

DB 21;

Indels 145; Length 1658;

Gaps

Conservative

1658 AA;

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CC The present invention specifically describes mammalian Esel and 2 CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein), vesicular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polynucleotide; agents that downregulate CC expression of Ese genes or antagonists of an Ese binding partner are CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of CC Esel is used to block clathrin-mediated endocytosis in vivo or in cell CC cultures, while administration of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal CC proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC cancer; abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Ese2I protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KALSPKKALLPPTVSLSATSTS-SQPPASVTDYHNV--SFSNLTVNT--
                                                                                                                                                                                                                                                                                                                                                                         -----QQKSAFTRTVSPG-SVSPTHGQGQAVENLKAQALCSWTAKKE
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MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ MAQFPTAMNGGPNMWAITSEERTKHDKQFDNLKPSGGYITGDQARTFFLQSGLPAPVLAE

187;

Indels

Gaps

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RESULT 14
RAY71160
ID AAY711
XX AAY71
XX AAY71
XX OB-SE
XX Rat;
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XX Cycli
                                                                                                                                                                                                                                                                                                                             The present sequence is a phosphodiesterase (PDE) interacting protein, CC M14 from rat. The protein modulates the functions and properties of PDEs, CC specifically CAMP-PDEs, and also targets them to specific subcellular CC compartments. The present sequence
CC can be used in the diagnosis and treatment of disease conditions
CC associated with PDE activity. The diseases include asthma, cystic CC fibrosis, inflammatory airway disease, chronic bronchitis, cosinophilic CC granuloma, psoriasis, proliferative skin disease, endotoxic shock, CC septic shock, ulcerative colitis, Crohn's disease, reperfusion injury, CC inflammatory airway disease, urticaria, adult respiratory CC distress syndrome, diabetes insipidus, allergic rhinitis, allergic conjunctivitis, vernal conjunctivitis, arterial restenosis, atheroselerosis, inflammatory diseases associated with irritation and CC atheroselerosis, inflammatory diseases associated with irritation and CC rejection and graft versus host disease conditions associated contitions of gastric acid, and disease conditions in which
              Query Match
Best Local S
Matches 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding a phosphodiesterase (PDE) interacting polypeptide, useful for diagnosis and treatment of asthma, cyfibrosis, Crohn's disease, and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; phosphodiesterase interacting protein; M14; PDE; cAMP-PDE; cyclic adenosine monophosphare whom we will be a composed to the composed to t
                                                                                                                                                                                                           Sequence
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fibrosis, Crohn's disease,
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analgesic; immunosuppressive; antiulcer; vasotropic; antiarthritic;
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tch 48.6%; al Similarity 50.8%; 652; Conservative 18
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              Score 3046; DB 21;
Pred. No. 1.1e-186;
7; Mismatches 267;
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EPGDLTFTEGEELLVTQKDGEWWTGSIGERTGIFPSNYVRPKDQENVGNASKSGASNKKP
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                                                                                                                KGWFPKSYVKLISGPVRKSTSIDTGPTES-PASLKRVASPAAKPAIPGEEFIAMYTYESS 1009
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Matches 603;
                                                                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 Primers useful for synthesizing use in genetic manipulation -
                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2647; 1380pp + sequence listing;
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B; Mismatches 20;
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Search completed: December Job time : 45 secs

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	GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	
OM protein - pro	OM protein - protein search, using sw model	
Run on:	December 4, 2003, 15:12:19 ; Search time 24 Seconds (without alignments) 4860.525 Million cell updates/sec	
Title: Perfect score:	US-09-674-237A-3	
Sequence:	1 MAQFPTPFGGSLDVWAITVEVGLFPSNYVKLTTDMDPSQQ 1213	
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	283308 seqs, 96168682 residues '	
Total number of	Total number of hits satisfying chosen parameters: 283308	
Minimum DB seq : Maximum DB seq :	Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing	Post-processing: Minimum Match 0%	

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	28	27	26	25	24	23	22	21	20	19	18	. 17	16	15	14	13	12	11	10	9	8	7	0	υī	4.	ω	2	_	No.	Result	
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ALIGNMENTS

417	358 RGNLELEKRRQALLEQQRKEQERLAQLERAEQERKERERQDQERKRQQDLEKQLEKQREL	Дb
418	ELEKRRQALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQL	β
	298 LPPEYIPPSFRRVRSGSGLSIMSSVSVDQRLPEEPEBEEPQNADKKLPVTFEDKKRENFE	ф
358	299 LPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFE	5
297	238 NLTGPQARTILMQSSLPQSQLATIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPI	뮍
7 298	-[2	δ
3 237	178 LPKSSSFGRSVAGSQINTKLQKAQSFDVPAPPLVVEWAVPSSSRLKYRQLFNSQDKTMSG	뭥
3 238	179 WPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSG	Ş
177	121 GIVGIPPLAAVAPVPMPSIPVVGMSPPLVSSVPTVPPLSNGAPAVIQSHPAFAH-SAT	Б
Г 178	119 GIASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAAT	8
8 120	61 IWALADMNNDGRMDQLEFSIAMKLIKLKLQGYPLPSILPSNMLKQPVAMPAAAVAGFGMS	뮍
3 118	EFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVA	γQ
2 60	1 MAQFGTPFGGNLDIWAITVEERAKHDQQFHGLKPTAGYITGDQARNFFLQSGLPQPVLAQ	DЬ
0 60	WAITVEERAKHDQQFLSLKPIAG	Ş
8	Query Match 80.8%; Score 5063.5; DB 2; Length 1270; Best Local Similarity 80.6%; Pred. No. 2.7e-198; Matches 980; Conservative 98; Mismatches 123; Indels 15; Gaps	, X m O
i, L.; Cesarenı five src homol	RESULT 1 T09194 T09194 C;Species: Xenopus laevis (African clawed frog) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: T09194 R;Yamabhai, M.; Hoffman, N.G.; Hardison, N.L.; McPherson, P.S.; Castagnoli, J. Biol. Chem. 273, 31401-31407, 1998 A;Title: Intersectin, a novel adaptor protein with two eps15 homology and fi A;Reference number: Z16605; MUID:99030416; PMID:9813051 A;Recession: T09194 A;Rocession: T09194 A;Rocession: T09194 A;Residues: 1-1270 <yam> A;Residues: 1-1270 <yam- a;description:="" a;experimental="" c;function:="" c;keywords:="" cell="" endocytosis="" endocytosis<="" in="" involved="" oocyte="" source:="" td="" type=""><td>CPLECUS PROCES OF TREES OF TRE</td></yam-></yam></yam></yam></yam></yam></yam>	CPLECUS PROCES OF TREES OF TRE

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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-C;Accession: T13055
R;Roos, J; Kelly, R.B.
J. Biol. Chem. 273, 19108-19119, 1998
A;Title: Dapi60, a neural-specific Eps15 homology and multiple SH3
A;Reference number: Z17594; MUID:98334647; PMID:9668096
A;Accession: T13055
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosidues: 1-1011 <ROO>
A;Cross-references: EMBL:AF054612; NID:g2996029; PID:g2996030; PID:
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Local Similarity 33.4%; Pred. No. 2.5e-63;
nes 413; Conservative 202; Mismatches 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               QQMLGRLIPEK-----QILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSPLD----PLKGI-VPAVAPVVPVVAPPVA--VATVISP-PGVSVPSGPTPPTSN---
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                    QQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPG
                                                                                                                                                                                                                                                                                                 NETSVSSAWDT - - -
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                                                                                                                                                                                                                                                                                                                                                          DKVENISKEIESKKEDINTNDVØMSELKAELSALITKCEDLYKEYDVØRTSVLELKYNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RORETEMEKEEORKRELEAKEAARKELEKOROOEWEOARTAEMNAOKEREOERVLKOKAH
                                                                                GQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLE
                                                                                                              PVAAV-EAPVDAQVADT
                                                                                                                                            PKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSA
                                                                                                                                                                                                    TIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKEVTDLTSAPA
                                                                                                                                                                                                                                                                EMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEI
                                                    -- ADLTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ŚVŚGVVSRPGSQPAŚRHASVSSQSGVGVVDADPTAGLPGQTSPEDKR
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                                                                                                                -YNDNINT-----SSIPAA
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664 757 693 697

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453

307 277 353 353 333 413 247

162

217

63 127 70

778

Qy 248 ILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPDEYIPPS 307	71 GRMDQVEFSIAMKLIKLKLOGYQLPSTLPPVMKQQPVALSAPAFGIGGIASMPPLT :	J. Biol. Chem. 273, 19108-19119, 1998 A;Title: Dap160, a neural-specific Eps15 homology and multiple SH3 domain-containing pro A;Reference number: Z17594; MUID:98334647; PMID:9668096 A;Recession: T13053 A;Recession: T13054 A;Recession: T13054 A;Recession: T13054 A;Recession: T13054 A;Residues: 1-1094 RROO> A;Residues: 1-1094 RROO A;Residues: 1-1094 RROO A;Residues: 1-1094 RROO A;Residues: 1-1094 RROO A;Residues:	Qy 1168 AFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYV 1202	7 9 10 10 11 11
RESULT 4 T31504 T31504 hypothetical protein Y116A8C.36 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T31504 R;McMurray, A. submitted to the EMBL Data Library, October 1999 A;Reference number: Z21041 A;Accession: T31504 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1097 <will a;cross-references:="" a;experimental="" cesp:y116a8c.36="" clone="" embl:al117204;="" pidn:cab55138.1;="" source:="" td="" y116a8c<=""><td>OY 1058TAGKTGSLGKKPEIAQVIASYAATGPEQLT 1087 </td><td> </td><td>624 NETSVSSAWDTGSSSAWEETGTTVTDPYAVASNDISALAAP 698 EMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEI 665 AVDLGGPAPEGFVKYQAVYEFNARNAEEI 758 TIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPA </td><td>Qy 474 RKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQES 533 </td></will>	OY 1058TAGKTGSLGKKPEIAQVIASYAATGPEQLT 1087		624 NETSVSSAWDTGSSSAWEETGTTVTDPYAVASNDISALAAP 698 EMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEI 665 AVDLGGPAPEGFVKYQAVYEFNARNAEEI 758 TIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPA	Qy 474 RKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQES 533

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C;Genetics:
A;Gene: CESP:Y116A8C.36
A;Introns: 50/3; 245/3; 411/3; 486/3; 697/1; 820/3; 926/2
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                                                                                                                                                                                                                                                                                         579
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                                AMGLTEGGA-----PPASSAPAAAAVIS-----QCIAQFQWRARNEEDLSFA
                                                                                                                                                          FESRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKP
||:|| ||::::| :| || ||| ||:::| :| | ||||
FEARSEDELSFEPGDVIIVFQSHAAEPGWRAGQLREKVGWFPEAFVEAIA--AVPTPG--
                                                                                                                                                                                                                                                                                                                                  LELSTEKEKSYNQTEILKTNKEKYKTDVYSK-----LVAKREEYRNSFEL---
                                                                                                                                                                                                                                                                                                                                                                                   -EVERETRSKLQEIDVF-NNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQ 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                LOESQOMLGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REBE---RRKEIERR-----EAAKRELE----RORQLEWERNRRQELLNQRNKEQEGTVV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKDGRLDIREYSIAMRLALNCLAGIPIPPQLPPSLLVVPA--RNAPPTWPGS------
   KSDVITVLEQQDMWWFG-EVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVA 987
                                                              QPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFN
                                                                                                                           VTDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAA
                                                                                                                                                                                                                          TDASQRFDADFGATST-----ADPFAQIAQAP--AHSKGAVDQSAFNIHDTYKCRALFA
                                                                                                                                                                                                                                                        KEAEERAKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYP 748
                                                                                                                                                                                                                                                                                       ---- LVHAQTHARSKI GEFEAKSAPASAAPAPAPAPATTTNGFPANFNDAFGEFD---K
                                                                                                                                                                                                                                                                                                                      KEDAQRRVQERDKQWLEHVQQEEQPRPRKP------HEEDRLKREDSVRK 688
                                                                                                                                                                                                                                                                                                                                                                                                                 LQETNQ---KTAIESQELGHQL--LQKQSAHKET-TQRKSELEALRKKDAIRKAIEDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REEEEKKRRLEMERRREEDEKMRKVQMEKAKVKQMQVQMPEQKKWNFYNQKQQENERLAQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELV-------RMCGISSRSANNTPELEPGAEPPQ--KSPAPKTFEDKRQDNLSKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSRHNSISAGSPLN-----NDRNVFEGRQLENWAIPHHNKLKYSQLFNALDKERLGSLS
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                                                                                               -----KAARKAEI-----AA
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Db QY	Qy Db	Qy Db	Db Qy	D _D	Фb	Qy Db	Query Ma Best Loc Matches	Db 874 AdAq Qy 1035 TVGD Db 934 RCNG :: Db 994 VGEI Qy 1150 VCQV Qy 1150 VCQV Db 1041RA RESULT 5 T34490 T34490 T34490 T34490 C;Accession: T3449 R;Aatreille, P. submitted to the E. A;Description: The A;Reference number A;Accession: T349 R;Status: prelimin A;Molecule type: D. A;Residues: 1.751 A;Cross-references A;Genetics: A;Genetics: A;Genetics: A;Genetics: ZX124 A;Map position: 2 A;Introns: 37/1; 7	Qy Qy
356 NFERGSVELEKRRQALLEQORKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQ 415	296 PPVLPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEDSSEDEQQPEKKLPVTFEDKKRE 355	236 MSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAWHLIDVAMSGQPL 295 :	177 -ATWPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKT 235	133 PMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPA 176	75 QVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPV 132	15 WAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMD 74	/ Match 8.1%; Score 506.5; DB 2; Length 751; Local Similarity 24.7%; Pred. No. 1.3e-13; 1es 214; Conservative 115; Mismatches 273; Indels 263; Gaps 34;	Db 874 kdAQYDVVSDVTLQASETAPQQQLYTVIDFPAVETTDLALHVGDTILVLEKNDEWWKG 933 Qy 1035 TVGDKSGVFPSNYVRLKDSEGSTAGKTGSLGKKPEIAQVIASYAATGPEQLTLA 1089 Db 934 RCNGREGIFPANYVEISVQQAGDFTPPTQAPTVLCEAKVVDFVASAPNQLGIK 993 QY 1090 PQQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPA 1149 Db 994 VGEITVIREKSAAGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPA 1149 QY 1150 VCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVQ 1095 RESULT 5 T34490 1041RATAVYDYEASQPDELGFKTGDVIIVTDKSEAEWWSGHREQDFSKSGLFPSNYVQ 1095 RESULT 5 T34490 R. Laterille P. Submitted to the EMBL Data Library, June 1995 A. Reference number: Z21534 A. Reference number: Z21534 A. Reference number: Z21534 A. References EMBL U29244; PIDN:AAC71084.1; GSPDB:GN00020; CESP:ZK1248.3 A. References: EMBL:U29244; PIDN:AAC71084.1; GSPDB:GN00020; CESP:ZK1248.3 A. Resperimental source: strain Bristol N2; clone ZK1248 A. Jacene: CISB:ZK1248.3 A. Jacen	815 KGDTIEVLEKQEMKWKGRNPAGEIGWFPKSYVKEVGATTSTTTPI-VSPSKASAGAPGAA 873 988 SPAAKPAIPGEEFIAMYTYESSEQGDLTFQQGDVIVYTKKDGDWWTG 1034

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C;Keywords: EF hand; phosphoprotein F;48-80/Domain: calmodulin repeat homology <EF1>F;160-192/Domain: calmodulin repeat homology <EF2>F;23-255/Domain: calmodulin repeat homology <EF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-897 <FRZ>
A;Cross-references: GB:L21768; NID:g404756;
C;Superfamily: calmodulin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: eps15, a novel tyrosine kinase substrate, exhibits A;Reference number: A54696; MUID:93361014; PMID:7689153 A;Accession: A54696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF receptor substrate eps15 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
C;Accession: A54696
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8; Mismatches 298;
                                                                                                                                                                                                                                                                                                    Score 486; Db 2,
     WVVSPAEKAKYDEIFLKTDKDMDGYVSGLEVRETFLKTGL
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuss; 1-96 < HERN
A;Cross-references: EMBL:Z29064; NID:g470034; PIDN:CAA82305.1; PID:g4
R;Wong, W.T.; Kraus, M.H.; Carlomagno, F.; Zelano, A.; Druck, T.; Crc
Oncogene 9, 1591-1597, 1994
A;Title: The human epsi5 gene, encoding a tyrosine kinase substrate,
A;Reference number: 138525; MUID:94239734; PMID:8183552
                                                                                                                                        R;Bernard, O.A.; Mauchauffe, M.; Mecucci, Concogene 9, 1039-1045, 1994
A;Title: A novel gene, AF-1p, fused to HRX
A;Reference number: S43074; MUID:94181254;
A;Accession: S43074
                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 01-Dec-2000
C;Accession: S43074; I38525
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PMID:8134107
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I.; Croce, C.M.; Huebner,
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A;Accession: 138525
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-821,'M',823-896 <RES>
A;Cross-references: EMBL:U07707; NID:9466259; PIDN:AAA52101.1; PID:9466260
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;Cross-references: GDB:360337; OMIM:600051
;Map position: 1p32-1p32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.7%; Score 485.5; DB 2; Length 896; Best Local Similarity 20.5%; Pred. No. 1.1e-12; Matches 198; Conservative 150; Mismatches 273; Indels 345;
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                                  781 ---ELKGKTGWFPAN-----YAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP
                                                                                                           739
                                                                                                                                                623
                                                                                                                                                                                                                                                                                                                                                                                                           554 VQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRS-----KLQEIDVFNNQLK 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                411 QLKEVRKKCAEEAQLISSLK-----AELTSQESQISTYEEELAK-----AREELSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 KLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQ 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 NTNLQKLQAQKQ-----QVQELLDE------------LDEQKAQLEE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 EAAKRELEROROLEWERNRROELLNORNKEQEGTVVLKARRKTLEFELEALNDKKHOLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 QORKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKORELEROREEERRKEIERR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 RDEFAVAMFLVYCALE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 WAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQFVLAQIWALADMNNDGRMD 74
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                                                                     TSV-----ETLKHNDPFAPGGTVVAASDSATDPFASVFGNESFGGGFADFSTLSKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQREK-----NNVEQDLKEKE-------DTIKQRTSEVQ---DLQDEVQRE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL 194
NEDPFRSATSSSVSNVVITKNVFEETSVKSEDEPPALP-----PKIGTPTRPCPLP
                                                                                                         KVVYYRALYPFESRSHDEITIQFGDIVMVDESQT-----GEPGWLGG------
                                                                                                                                              DPFVGSDPFKDDPFGKIDPFGGDPFKGSDPFASDCFFRQSTDPFATSSTDPFSAANNSSI
                                                                                                                                                                                -----AKPEMQDKQSRLFHPHQEPAK------LATQAPWSTTEKGPLTISAQESV
                                                                                                                                                                                                                       VTDENEVTTAVTEKVCSELDN------NRHSKEEDPFNVDSSSLTGPVADTNLDFFQS
                                                                                                                                                                                                                                                         EKOKEDAORRVOERDKOWLEHVOOEEOPRPRKPHEEDRLKREDSVRKKEAEER------
                                                                                                                                                                                                                                                                                                WCSSPHSILVNGATDYCSLSTSSSETANLNEHVEGQSNLESEPIHQESPARSSPELLPSG
                                                                                                                                                                                                                                                                                                                                ELREIHS-----KQQLQKQRSLEAARLKQKEQERKSLEL----
                                                                                                                                                                                                                                                                                                                                                                       LQQETAE-----LEESVESGKAQLEPLQQHLQDSQQEISSMQMKLMEMKDLENHNSQLN
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Qy 124PPLTAVAPVPM- :	Qy 105QPVAI	Qy 76 VEFSIAMKLIKIKLÇ :: Db 326 PEFALAMHLINDVLC	Qy 17 ITVEERAKHDQQFLS ::: : Db 266 ITAQDQAKFETLFRS	Query Match Best Local Similarity 20.5%; Matches 261; Conservative 1	poly(A) - specific ribonuclease (EC 3.1.13.4) - yeast N; Alternate names: protein YIB6c; protein YIR006c C; Species: Saccharomyces cerevisiae c; Date: 02-Dec-1994 Hsequence revision 02-Dec-1994 C; Accession: \$48440; \$30889; \$58706; \$50795; \$27447; R; Badcock, K.; Churcher, C. submitted to the EMBL Data Library, August 1994 A; Reference number: \$48432 A; Accession: \$48440 A; Residues: 1-1480 < BAD> A; Residues: 1-1234, 'T.; 236-265, 'YYCPRSGKW', 274-479, 'A; Residues: 1-234, 'T.; 236-265, 'YYCPRSGKW', 274-479, 'A; Cross, -references: EMBL.M90688; NID:9172095; PIDN: R; Voss, H.; Tamames, J.; Teodoru, C.; Valencia, A.; Yeast 11, 61-78, 1995 A; Cross-references: EMBL.X79743 R; Voss, H.; Tamames, J.; Teodoru, C.; Valencia, A.; Yeast 11, 61-78, 1995 A; Title: Nucleotide sequence and analysis of the call the color of the call the call the color of the call	831 786 866 846
PPLTAVAPVPMGSIP-VVGMSPPLVSSVPPAAVPPLAN 160 		VEFSIAMKLIKLKLQGYQLPSTLPPVMKQ	ITVEERAKHDQQFLSLKPI-AGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMDQ 75	.5%; Score 410.5; DB 2; Length 1480; .5%; Pred. No. 2.1e-09; e 174; Mismatches 444; Indels 395; Gaps 47;	se (EC 3.1.13.4) - yeast (Saccharomyces cerevisiae) YIB6C; protein YIR006C revisiae revisiae	VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDT 865

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PIPPSVTQEPPVPLAPPLPAVDGFQEPPIPSAPAIATAVQKSGSSTPALAGGVLPPP---
                                                                                                                                                                                                                                                                                                                   STWPSSSNE----KPETDNWDTWAAQPSLTVPSAGQLRQRS-AFTPATATGSSPSPVLG
                                                                                                                                                                                                                                                                                                                                                                                DNKVEEAKIGHPDHARAPPV---TAAPLPSV----TPVPPAVPVPQANTSNEKSSPIPIA 1345
                                                                                                                                                                                                                                                                                                                                                                                                                       AEKIPENEVPTP----AKPVTDLTSAPAPKLALRETPAP--LPVTSSEPSTTPNNWADFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFGGHVNVPQAAPVAPSAAFSQNSTNAPRSVHAAVTPAAGKNSTGLPSTTMGHNPYFKDA 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAKQESDDEDEDDEEKRLQEELKRLKKKKADKEKRLAALRKQIEDAQNESDEEETNGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RATPFQEEKYVÉVÁQPTQÞVQSTQÞVQÞTQÞVQÞTQÞVQÞTQÞVQÞTQPVQÞTQPVQNVY 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFN--NQLKELREIHSKQQL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEKQLEKQRELERQREEERRKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QESVKVVYYRALYPPESRSHD-EITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKR-----EDSVRKKEAEE----
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                                                                                                                                                                                                       QGEKVEGLQAQALYPWRAKKDNHLNFNK-----SDVITVLEQQDMWWFGEVQGQK 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDK----KRENFERGSVELEKR
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                                                                                                                                                   --PPLPTQQASTSEPIIAHVDNYNGAEKGTGAYGSDSDDDVLSIPES--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --STSTFDARAAEMORRIORG----LDEDE--DDGWSDEDESNNR----VAV 1292
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C;Keywords: calcium binding; EF hand; transmembrane protein
F;167-199/Domain: calmodulin repeat homology <EF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
C; Superfamily: )
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A;Experimental source: strain S288C
R;Scherens, B.; el Bakkoury, M.; Vierendeels, F.; Dubois, E.; Messenguy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain S288C
R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy,
submitted to the Protein Sequence Database, August 1994
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N;Alternate names: hypothetical protein YBL0520
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 19-Apr-2002
C;Accession: S45781; S50284; S45782; S39841; S37339; S42498
R;Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; vsubmitted to the Protein Sequence Database, August 1994
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A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left A;Reference number: S39824; MUID:94205266; PMID:8154187
A;Accession: S39841
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A;Title: The sequence of a 22.4 kb DNA
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A; Residues: 579-1381 <SCH>
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A; Residues: 579-1381 < DUB>
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A; Accession: S45782
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A; Residues: 1-961 < DEF>
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Matches 286
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Residues: 1-961 <GOF>
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                                                         GVSSLTRHSTISRLSTGAFSNA-
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TMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQP
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20.0%; Pred. No. 4e-09;
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1072 AQVIASYAATGÞEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFÞANYVKLLS 	1021 VIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSL 	966VRKSTSIDTGPTESPASLKRVASPAAKPAIPGEEFIAM	924HLNFNKSDVITVLEQQDMMWFGEVQGQKGWFPKSYVKLISGP : : : : : : : : : : : : : :	870 PSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDN-	810 TDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWDAQ	758 TIQPGDI-VMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTP-A :	714ACLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEI	664 QQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLF : : : :	609 LREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHV	549 DQLKQVQQNSLHRDSLJTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFNNQLKE	493 GKLQDIRCRLATQRQBIESTNKSRELRIABITHL	433 REAAKRELERORQLEWERNRROELLNORNKEOEGTVVLKARRKTLEFELEALNDKKHQLE	383AQLERAEQERKERERQEQEAKRQLELEKQLEKQRELERQREEERRKEIE	527 SPVKRTASTTLPQVPNFSVFSMPAGAATSAATGAAVGAAVGAAALGAS	342 EKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERL :	325 VDQRLPEEPS	295 LPPVLPPEYIPPSFRRVRSGSGMSVISSSS	: : 291 QHAGSLSSAVLVPFFLSSRLNQETLATIWDLADIHNNAEFTKLEFAI
elqargkkrqigwfpanyvkilsp 1131 :	GSGTAGKTGSLGKKPEI 1071 	GEEFIAMYTYESSEQGDLTFQQGD 1020 	FPKSYVKLISGP 965	-QGEKVEGLQAQALYPWRAKKDN- 923 	FSSTWPSSSNEKPETDNWDTWAAQ 869 	YAEKIPENEVPTP-AKPV 809 : : : : : : : : :	AQESVKVVYYRALYPFESRSHDEI 757	PEMODKOSRLFHDHOEP 713 ::: YANNVRELSEROMNL-AMGOLPED 890	EKOKEDAQRRVQERDKOWLEHV 663 : :: :: : DREKOLEERNRQIEEQENLYHQHV 837	LDEVERETRSKLQEIDVFNNQLKE 608 : : : : IDGLGEKISVYLTKQKE 783	THLQQQLQESQQMLGRLIPEKQILS 548	VLKARRKTLEFELEALNDKKHQLE 492	EKQLEKORELEROREEERRKEIER 432 	AFSRSSNNAFKN	QRKEQERL	SEDEQQP 341 	SSS 324 : RASKPSLQDMPHQVSAPAVNTQPT 410	: : : : NAEFTKLEFAIAMFLIQKKNAGVE 350

;	Db	Ş	Db	Ş	DЬ	Q	В	Q	מם	Ş	Db	Q	Дb	Q	Дb	<i>Q</i>	Query M Best Lo Matches	A; Intro C; Super C; Keywo F; 49-81	A;Cross-ref C;Comment: Covalent mc C:Genetics:	A;Accession A;Molecule A;Residues	submitt A;Descr A;Refer	C;Accession: R;Fietz, M.J	trichohyalir C;Species: C C;Date: 12-N	RESULT	В	φ.	DЬ
	612 LLOEREBERLRROERERKLREEEO 635	680 LKREDSVRKKEAEERAKPEMQ 700	553 LQREKRRQ-EREREYREEEKLQREEDEKRRRQERERQYRELEELRQEEQLRDRKLREEEQ 611	QKEQERKSLELEKQKEDAQRRVQERDKQWLEH	493 RAQQLQEEDSFQEDRERRRRQQEQRPGQTWRWQLQEEAQRRRHTLYAKPGQQEQLREEEE 552	RETRSKLQEIDVFNNQLKELREIHSKQQLQK	433 EESERRORLSARPSIRERQIRAEERQEQEQRFREEEEGRRERRQEIQFIEEEEGQQRREE 492	QMLGRLIPEKQIL	377 ORQLESEAGAROSKVYSRPRRQEEQSLRODQERRQRQERERELEEQARROQOWQAE 432	TLEFELEALNDKKHQLEGKLQDIRCRLATQ	318 RREQRIEQEERREQQLKRELEEIREREQRIEQE-ERREQLIAEEVREQARERGESITRRW 376	427 RKEIERRE-AAKRELERQROLEWERNRRQELLNQRNKEQEGTVVLKAR 473	258 QLRRELEBIREREQRIEQEERREQQLRREQRIEQEERREQQLRRELEBIREREQRIEQEE 317	EQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQRELERQRE	198 EEFIEEEQLRRREQQELKRELREEEQQRRERREQHERALQEEEEQLLRQRRWREEPREQQ 257	326 DQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQ 375	, Match 6.2%; Score 391.5; DB 1; Length 1407; Local Similarity 29.7%; Pred. No. 1.2e-08; Les 132; Conservative 97; Mismatches 140; Indels 75; Gaps 18;	A;Introns: 46/3 A;Introns: 46/3 C;Superfamily: trichohyalin; calmodulin repeat homology C;Reywords: calcium binding; citrulline; EF hand; hair; tandem repeat F;49-81/Domain: calmodulin repeat homology <ef2></ef2>	A;Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747 C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she Covalent modifications to this protein include conversion of arginine to citrulline and t	A;Accession: S28589 A;Molecule type: DNA A;Residues: 1-1407 <fie></fie>	d to the ption:	: S28589 J.; Rogers, G.E.	₹ C p	10	1296 GNSKAEPTKVATPSIPQQPIPLKNDPIVDASLSKGPIVN 1334	LPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQI	1273 QQ QSTSDPAQVSNDEWD-EIFAGF 1295

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RESULT 11
A45592
Liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)
Liver stage antigen falciparum
C;Species: Plasmodium falciparum
C;Date: 22-Nov-1993 #sequence revision 02-Dec-1994 #text change 09-Jun-2000
C;Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592
R;Zhu, J.; Hollingdale, M.

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submitted to the EMBL Data Library, April 1992
A; Description: a liver-stage-sepcific antigen of plasmodium fals:
A;Accession: S34842
A;Accession: S34842
A;Status: nralisimuski description: nralisimuski description: nralisimuski description: nralisimuski description: S4842
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 323-381, 'HKAI' <GUE2>
A;Cross-references: EMBL:M28266
A;Otoe: difference at carboxyl end due to frameshift error C;Comment: This protein is found as flocculent material in C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: EF hand
C;Keywords: F hand
C;Keywo
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Nature 329, 164-167, 1987
A;Title: A liver-stage-specific antigen of Plasmodium falciparum characterized by A;Reference number: $29393; MUID:87315391; PMID:3306406
A;Accession: $29393
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A;Reference number: $24597
A;Accession: $24597
A;Molecule type: DNA
A;Residues: 1-1909 <ZHU>
A;Cross-references: EMBL:X56203; NID:g9915; PID:g9916
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MOl. Biochem. Parasitchl. 48, 223-226, 1991
A;Title: Structure of Plasmodium falciparum liver stage
A;Reference number: A45592; MUID:92107224; PMID:1840628
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                                                                                                                                        RLAKEKLOEQOSDLEQERRAKEKLOEQOSDLEQDRLAKEKLOEQORDLEQERRAKEKLOE
                                                                                                                                                                                                                                                                                                                                                           LKARRKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQ 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELERORE-----EERRKEIERREAAKREL-EROROLEWERNRRQELLNORNK-EOEGTVV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KETLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLQEQQS-DLEQERLAKEKLQEQQSDLEQERLAKE-----KLQG------QQSDLEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VELEKRRQALLEQQRKEQERL-AQLERAEQERKERER-QEQEA---KRQLELEKQLEKQR 416
                                                                QLDEVERETRS--KLQEIDVFNNQLKEL-REIHSKQQLQKQRS--LEAARLKQKEQERKS
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                                                                                                                                                                                                                LOESOOMLGRLIPEKQILSDOLKQVQQNSLHRDSLLTLKRALEAKELARQQLRE
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28.3%; Pred. No. 3.6e-08;
tive 113; Mismatches 198
- QQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQS
                                                                                                                                                                                                                                                                                    -LQEQQSDLEQERRAKEKLQEQQSDLEQE
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A;Molecule type: DNA
A;Residues: 1-1898 <-LEB>
A;Residues: 1-1898 <-LEB>
A;Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root
C;Covalent modifications to this protein include conversion of arginine to citrulline ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
A45973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: calcium binding; citrulline; EF hand; hair; tandem F;49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A45973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, J. Biol. Chem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a full ed (cross-linking) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trichohyalin - human
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DORLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQ--RKEQE--R
                                                                                                                                                                                                                                       LREQUIDE-VERETRSKLQEIDVFNNQLKELR----EIHSKQQLQKQRSL----EAARLKQK
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PQEQEEKRRESELQWQEEERAHRQQQEEEQRRDFTWQWQAE-----EKSERGRQRLS
                                               PHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTIS
                                                                                              LKREHEEERREQELAEEEQEQARERIKSRIPKWQWQLESEADARQSKVLLEAPQAGRAEA
                                                                                                                                                                                          QEERRDERLKREEPEEERRHELLKSEEQEERRHEQLRREQQERREQRLKREEEEERLEQR
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                                                                                                                                           -----EQERKSLEL-EKQKEDAQRRVQERDKOWLEHVQQEEQPRPRK-------
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Pred. No. 4.5e-08;
17; Mismatches 154
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AQESVKVVYYRALYPFESRSHDE 756

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RESULT
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C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair;
F;49-81/Domain: calmodulin repeat homology <EF2>
F;387-851/Region: 28-residue repeats
F;387-851/region: 73-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Sep-1993 #sequence revision 01-Mar-1996 #text_change 22-Jun-1999
C;Accession: A40691; A34209; S32633
R;Fietz, M.J.; McLaughlan, C.J.; Campbell, M.T.; Rogers, G.E.
J. Cell Biol. 121, 855-865, 1993
A;Title: Analysis of the sheep trichohyalin gene: potential structural and A;Reference number: A40691; MUID:93260018; PMID:7684041
A;Accession: A40691; MUID:93260018; PMID:7684041
A;Accession: A40691; MUID:93260018; PMID:7684041
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A;Cross-references: GB:X51695; NID:91827; PIDN:CAA35992.1; PID:91828
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she covalent modifications to this protein include conversion of arginine to citrulline and
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A;Cross-references: RMBL:Z18361; NID:g295940; PIDN:CAA79165.1; IA;Cross-references: RMBL:Z18361; NID:g295940; PIDN:CAA79165.1; IA;Cross-references: RMBL:Z18361; NCBI backbone (NCBIP:132511)
A;Fietz, M.J.; Presland, R.B.; Rogers, G.E.
J. Cell Biol. 110, 427-436, 1990
A;Title: The cDNA-deduced amino acid sequence for trichohyalin, A;Reference number: A34209; MUID:90130632; PMID:2298812
A;Accession: A34209
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Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                            QLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEK-----
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                                                                             RROEREROYLEKEELOROEE----RLOREKEQLOREDREKRROVRERKYLEEELOGEEDRL
                                                                                                                   RVQERDKQWL--EHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER--AKPEMQDKQSRL 706
                                                                                                                                                          QERERQYLEKELQRQEERLQEEEQLLREEREKRRQERERQYLEKVELQEEEQLQREEREK
                                                                                                                                                                                                                                                                          QILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFNN 604
                                                                                                                                                                                                                                                                                                                                                     KKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQ--QQLQESQQMLGRLIPEK 544
                                                                                                                                                                                                                                                                                                                                                                                                                                RKEIERRAAKRELEROROLEWERNRROELLNORNKEOEGTVVLKARRKTLEFELEALND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEQERKERERQ------EQEAKRQLELEKQ-----LEKQRELERQREEER
                                                                                                                                                                                                                                   QYL-EKVELQEEEQLQRQEREKRRQERERQYLEKVELQEE-EQVQRQEREK-----RR
                                                                                                                                                                                                                                                                                                                                                                                         ROERERQYLEKVELQEEEQLQREEREK----RRQERE-----
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                                                                                                                                                                                                                                                                                                                -KVELQEEEQ------LQRQEREKRRQEREKQYLEKVELQEEEQLQRQERQKRRQEREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 375.5; DB 1; ilarity 27.6%; Pred. No. 5.9e-08; Conservative 101; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-residue repeats
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  QPMYYTTREPEVTTKVERQVIERIDRNVWVEDVPYAPSQS
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RyFavello, T.

RyFavello, T.

Submitted to the EMBL Data Library, Octobe submitted to the sequence of C. elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U39650; NID:g1049376; PID:g1049381; PIDN:AAA80392.1; CESP:C25A11
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z18375
A; Accession: T15597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 MSG--HLTGPQARTILMQS--SLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNS-----HDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSKQQLQKQRSL-EAARLKQKEQERKSL---ELEKQKEDAQRRVQERDKQWLEHVQQEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRQLEWERNRRQ----ELLNQRNKEQEGTV---VLKARRKTLEFELEALNDKKHQLEGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REKKRREEWDRLESIRLAEEEAELARRRALEKER-IDREKAEEERKTMERLERERARLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPEKKLPVTFEDKKRENFERGSVELEKRRQ-----ALLEQQRKEQERLAQLERAEQER
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APLPVTSSEPSTTP--
                                                                                                             VDESQTGEPGWLGGELKGKTGWFPANYAEKI PENEVPTPAKPVTDLTSAPAPKLALRETP
                                                                                                                                                                         RERANEEAOLADLLERERHNOLIRENERREAVERANNRRLE--DRRSRDKL-----DHIV
                                                                                                                                                                                                                              FHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVM
                                                                                                                                                                                                                                                                                       KRRQEEEEEIARLNELQRAAAARQAQRNAELDRQRQRDELDRK-AQELSEREMREKERRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSISSSREDLLSEHATSRSTVREIPVHRAPSTAP---SHSSVFEYHMMPTTTSTYHHVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88/3; 126/3; 433/2; 494/2; 711/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 142; Mismatches 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 359.5; DB 2;
Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
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legans cosmid
                                                           FELEKRRLLAEKEAMNRKK--NHLLSSE----TLAKLT
                                                                                                                                                                                                                                                                                                                                               -----DRLKREDSVRKKEAEERAKPEMQDKQSRL
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  NNWADFSSTWPSSS
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826 643	VDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETP	767 604	B 8
603 .	RERANESAQLADILERERHNQLIRENERREAVERANNRRLEDRRSRDKLDHIV	551	밁
766	LATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVM	707	S
706 550	PRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRL : : : : : : : : :	492	용 성
491	ERKEEERREFELIBAARRKKEARDRDRLDEMERERVREEEERREKERREQERRIAAEKER	432	₽
899	QCLQKQRSL-EAARLKQKEQERKSLELEKQKEDAQRRVQBRDKQWLEHVQQEEQ	613	Ş
612 431	-QQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFNNQL-KELREI :: :: :: :: :: RRREEERREAELVADVHRQAEERERLRKRQEREEAERLERIRLEQQKIDMERIDAERRER	555 372	B 8
371	RLLRERLELERIERERRELEARERQELELQRREAEDRERQRLEDEAREM	323	₽ \$
· N	ERRÉHÉRIEIERIKŘERIERÉRREREEKKAEED	267	₽
495	LEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALNDKKHQLEGKL	443	Q.
442 266	KERERQEQEAKRQLELEKQLEKQRELERQREEERRKEIERREAAKRELER : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	393 208	용 성
392 207	QPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERLAQLERAEQER	340 149	유 성
339 148	GQPLPPVLPPEYIP-PSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQ	292 92	B 8
291 . 91	MSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMS	236 64	유 성
235 63	KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKT	181 7	용 성
32;	5.7%; Score 359.5; DB 2; Length 1017; Similarity 23.6%; Pred. No. 1.6e-07; 9; Conservative 142; Mismatches 270; Indels 169; Gaps	Query Match Best Local S Matches 179	≩ ñ Ó
1; CESP:C25	innary; translated from GB/EMBL/DDBJ: DNA 1017 <fav> 017 <fav> ces: EMBL:U39650; NID:g1049376; PID:g1049380; PIDN:AAA80391. source: strain Bristol N2 5A11.4a ; 88/3; 126/3; 433/2; 494/2; 711/2; 735/1; 792/3; 833/3; 873</fav></fav>	Status: prelimina Molecule type: DM Residues: 1-1017 Cross-references: Experimental sour Genetics: Gene: CESP:C25A11 Introns: 65/3; 88	A A C A A A A A A A A A A A A A A A A A
	o the EMBL Data Library, October 1995 on: The sequence of C. elegans cosmid C25All. number: Z18375 : T15598	submitted to the A;Description: T A;Reference numb A;Accession: T15	sub A;D A;R
-	:al protein C25All.4a - Caenorhabditis elegans : Caenorhabditis elegans)-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 on: T15598	RESULT 15 T15598 hypothetical pr C;Species: Caen C;Date: 20-Sep- C;Accession: T1 D:Faresion: T1	RESI T15 C;S C;D

Search	DЬ	Qy
completed:	644 Q	827 A
ä.	YAWA	, P VaTa'
December	YYTTREPEVTTKVERQV	PVTSSEPSTTP
4	TKV	P
4, 2003,		
15:20:53	IERIDRNV	MNN
53	WVEDVPYAP	ADFSST
	APSQS	SSSAM
	683	854

Search completed: December 4, 2003, 15:20:53
Job time: 31 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     5842.5

5063.5

5063.5

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Pfam; PF00018; SH3; 5.

PRINTS; PR00452; SH3DOMAIN.

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SMART; SM00023; EFh; 2.

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2 EH domains.
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EH 2.

EF + HAND 2 (POTENTIAL).

LYS/LEU/GLU/ARG/GLN-RICH ()

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SH3 1.

SH3 2.

SH3 3.

SH3 4.

SH3 5.

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LPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSN
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                       TGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTE
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                Pfam; PF00036; efhand; 3. Pfam; PF00018; SH3; 5. ProDom; PD000066; SH3; 5.
                                                                                             EMBL; AF127798; AAD30271.1; -. EMBL; AF132672; AAD31026.1; -. HSSP; P29354; IGFC.
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Okamoto M., Schoch S., Suedhof T.C.;
"EHSH1/intersectin, a protein that contains EH and
binds to dynamin and SNAP-25. A protein connection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Intersectin 1 (EH domain and SH3 domain regulator of endocytosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9WVE9; Q9WV
28-FEB-2003
                                                        InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
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                                                                                                                                                 ween the Swiss Institute of Bioinformat
European Bioinformatics Institute. The
by non-profit institutions as long
ified and this statement is not removed.
ities requires a license agreement (See
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        bind to dynamin.

DOWAIN: The KLERQ domain binds to Sh
SIMILARITY: Contains 2 EP-hand calci
SIMILARITY: Contains 5 SH3 domains.
SIMILARITY: Contains 2 EH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 274:18446-18454(1999).

FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery. May regulate the formation of clathrin-coated vesicles.

SUBUNIT: Interacts with dynamin, SNAP-25 and SNAP-23. Clusters several dynamin in a manner that is regulated by alternative splicing. Also binds clathrin-associated proteins and other components of the endocytic machinery, such as N-WASP, Eps15 and solutions.
                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFION DOMAIN: SH3-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stonin 2 (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated protein Enriched in synaptosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocytosis?";
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                                                                                                                                                                                                                                                                                                                            IsoId=Q9WVE9-2; Sequence=VSP_004297; SSUE SPECIFICITY: Highly expressed in MAIN: SH3-3, SH3-4 and SH3-5, but not
                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9WVE9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                            Comment=Additional isoforms
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SM00326; SH3; 5.

; PS00018; EF HAND;

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EHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAKLATQA
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EF 1.

EF -HAND 1 (POTENTIAL).

EH 2.

EF 2.

EF-HAND 2 (POTENTIAL).

LYS/LEU/GLU/ARG/GLN-RICH (COILED COIL (POTENTIAL).

SH3 1.

SH3 2.

SH3 3.

SH3 4.

SH3 4.

SH3 5.

POLY-SER.

Missing (in isoform 2).

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(1581; O95216; Q9UET5; Q9UK60; Q9UNK1; Q9UNK2;

(01-NOV-1997 (Rel. 35, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Intersectin 1 (SH3 domain-containing protein 1A)
                                                                                                                                  Pucharcos C., Fuentes J.-J., Casas C., de la Luna S., Alcanta: Arbones M.L., Soriano E., Estivill X., Pritchard M.; "Alu-splice cloning of human intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome."; Eur. J. Hum. Genet. 7:704-712(1999).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=99415290; PubMed=10482960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two isoforms of a human intersectin (ITSN) protein are produced brain-specific alternative splicing in a stop codon."; Genomics 53:369-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guipponi M., Scott
Antonarakis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Fetal brain;
TISSUE=Fetal brain;
MEDLINE=99017974; PubMed=9799604;
MCDLINE=99017974; PubMed=9799604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                SEQUENCE OF
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Cytogenet. Cell Genet. 78:213-215(1997).

-i-FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery. May regulate the formation of clathrin-coated vesicles. Isoform 1 could be involved in brain-specific synaptic vesicle recycling.

-i-SUBUNIT: Interacts with dynamin, SNAP-25 and SNAP-23. Clusters several dynamin in a manner that is regulated by alternative splicing. Also binds clathrin-associated proteins and other components of the endocytic machinery, such as N-WASp, Eps15 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pucharcos C., Casas C., Nadal M., Estiv
"The human intersectin genes and their
differentially expressed.";
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Tassone F., Rynditch A.V., Gardiner K.;
"Mouse homologs of human chromosome 21 genes."
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98127038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENE MAPPING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparks A.B., Hoffman N.G., McConnell S. "Cloning of ligand targets: systematic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98294438;
                                                            SIMILARITY: Contains 1 DBL-homology (DH) domain SIMILARITY: Contains 2 EF-hand calcium-binding SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 5 SH3 domains. SIMILARITY: Contains 5 SH3 domains.
                                                                                                                                                                                                                           IsoId=Q15811-4; Sequence=VSP 004294;
TISSUE SPECIFICITY: Ubiquitous in adult and fetal tissues, excision 1 which is expressed almost exclusively in the brain. Highly expressed in skeletal muscle, heart, spleen, ovary, tes and all fetal tissues tested. Expressed at lower levels in thy blood, lung, liver and pancreas. Isoform 1 is expressed in all brain regions; not expressed in the spinal cord.

DOMAIN: $H3-3, $H3-4 and $H3-5 but not $H3-1 and $H3-2 domains bind to dynamin (By similarity).

DOMAIN: The KLERQ domain binds to SNAP-25 and SNAP-23 (By
                                                                                                                                                                                               similarity)
DISEASE: Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing; Named isoforms-4;
Comment-Additional isoforms seem to exist. Alternative splicing
affects domains involved in protein recognition and thus may
play a role in selecting specific interactions;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1; Synonyms=Long, ITSN-1; IsoId=Q15811-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enriched in synaptosomes ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stonin 2 (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated
                                                                                                                                                 SIMILARITY: Contains 1 C2 domain.
                                                                                                                                                              suggesting a gene dosage-depend
abnormalities of Down syndrome
                                                                                                                                                                                                                                                                                                                                                                                                  Name=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H., Antonarakis S.E.;
SH3D1A gene maps to human chromosome 21q22.1-->q22.2.";
genet. Cell Genet. 78:213-215(1997).
                                                                                                                                                                                                                                                                                                                                                                                                           ame=2; Synonyms=Short, ITSN-8;
IsoId=Q15811-2; Sequence=VSP_004295;
ame=3; Synonyms=Short 2, SH3PI7;
IsoId=Q15811-3; Sequence=VSP_004293,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biophys. Acta 1521:1-11(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marrow;
                                                                                                                                                                                                 Overexpressed in brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9630982;
                                                                                                                                                                                dosage-dependent
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_004293, VSP_004294,
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EMBL; AF064244; AAC78611.1; -...
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EF-HAND 1 (POTENTIAL).
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EF-HAND 2 (POTENTIAL).
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SH3 1.
SH3 2.
SH3 3.
SH3 4.
SH3 5.
DH.
C2 DOMAIN.
Missing (in isoform 3).
/FTId=VSP 004293.
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P -> A (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                           Pfam; PF00036; efhand; 2.
Pfam; PF00018; SH3; 5.
PRINTS; PR00499; PF67PHOX.
PRINTS; PR00452; SH3JOMAIN.
ProDom; PD000666; SH3; 5.
                                                                                                       PIR; T09194; T09194.

HSSP; P29355; 1SEM.

InterPro; IPR002048; EF-hand.

InterPro; IPR000261; EPS15_homology.

InterPro; IPR000108; Neu_Cyt_fact_2.

InterPro; IPR001452; SH3.
                                                                                                                                                                                   EMBL; AF032118; AAC73068.1; PIR; T09194; T09194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99030416; PubMed=9813051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae;
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SM00054; EFh; 2.
SM00027; EH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGT 1133
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PROSITE; PS00018; EF_HAND;
PROSITE; PS50031; EH; 2.
PROSITE; PS50002; SH3; 5.
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                                                           RLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQE
                                                                                                                                                                                                                                                                                                                                 ERQREEERRKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKARRKTLE
                                                                                                                                                                                                                                                                                                                                                                                                QIPWMNTEKAPLTIN-QGDVKVVYYRALYPFDARSHDEITIEPGDIIMVDESQTGEPGWL
                    QAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWL
                                                                                                                         FELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLG
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BF-HAND 1 (POTENTIAL).

EH 2.

EH 2.

EF-HAND 2 (POTENTIAL).

LYS/LEU/GLU/ARG/GIN-RICH (
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SH3 1.

SH3 3.

SH3 4.

SH3 5.
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Pred. No. 2.56
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TISSUE=Fetal brain, and Fetal liver;
MEDLINE=20382722; PubMed=10922467;
Pucharcos C., Estivill X., de la Luna
"Intersectin 2, a new multimodular pro
mediated endocytosis.";
FEBS Lett 478.42
                                                                                                                                                                                                                                                                                                                                                                                                            ONNZM3; O95062; Q15812; Q9HAK4; Q9NXE6; Q9N
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Intersectin 2 (SH3 domain-containing protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                        Seifert M., Engel M., Welter C.;
"Intersectin 2 (SH3D1B), human homolog of mouse Ese2 pro
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                               FEBS
 SEQUENCE
                                                                               Ohara O.
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                         "Prediction of the coding se
The complete sequences of 10
for large proteins in vitro.
DNA Res. 6:337-345(1999).
                                                                                         MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K.-I., Kikuno
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       WASP associated protein).
ITSN2 OR SH3D1B OR SWAP OR KIAA1256.
                                                                                                                      FISSUE=Brain;
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 258-720
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FROM N.A.
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                                      sequences of unidentified 100 new cDNA clones from bro.";
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IsoId=Q9NZM3-2; Sequence=VSP_003892;
Name=3; Synonyms=TTSN2-S1;
IsoId=Q9NZM3-3; Sequence=VSP_003893, VSP_003894;
Name=4; Synonyms=TTSN2-S2; SH3P18;
IsoId=Q9NZM3-4; Sequence=VSP_003895;
IsoId=Q9NZM3-4; Sequence=VSP_003895;
IsoId=Q9NZM3-4; Sequence=VSP_003895;
IsoSUB SPECIFICITY: Ubiquitous. Isoform 1 is primarily expression adult heart and liver.
In adult heart and liver.
IMISCELLANEOUS: Overexpression results in the inhibition of the transferrin uptake and the blockage of the clathrin-mediated
             EMBL;
EMBL;
                                                        EMBL;
                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                   -!- FUNCTION: Adapter protein that may provide indirect lin the endocytic membrane traffic and the actin assembly membrane traffic and the actin desembly membrane traffic and the cotin content was regulate the formation of clathrin-coated vesicles.
-!- SUBUNIT: Belongs to a complex that may contain multimer ITSN2 and Eps15, and different partners according to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain, and Fetal liver;
MEDLINE=21548828; PubMed=11690630;
Pucharcos C., Casas C., Nadal M., Estivill X.,
"The human intersectin genes and their spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparks A.B., Hoffman N.G., McConn
"Cloning of ligand targets: system
containing proteins.";
Nat. Biotechnol. 14:741-744 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 821-1284 FROM N.A. (ISOFORM 1). Wilson L.A., Fields D., Cruz L., Friesen J., & "SH3P18-like wasp associated protein (SMAP): // containing protein that interacts with WASP." Submitted (APR-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentially expressed.";
Biochim. Biophys. Acta 1521:1-11(2001).
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TISSUE=Embryo;
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SUBCELLULAR LOCATION: Cytoplasmic
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing; Named isoforms-4; Comment-Additional isoforms seem to exist; Name-1, Synonyms=ITSN2-L; IsoId=Q9NZM3-1; Sequence=Displayed;
             AF182199;
AF248540;
AB033082;
                                                            AF182198; AAF59903.1;
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             AAF59904.1;
AAF63600.1;
BAA86570.1;
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man N.G., McConnell S.J., Fowlkes I
d targets: systematic isolation of
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; ALT_INIT.
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SMART; SM00024; EFh; 2.
SWART; SM00027; EH; 2.
SWART; SM00027; EH; 2.
SWART; SM00236; SH3; 5.
SWART; SM00326; SH3; 5.
SWART; SM00326; SH3; 5.
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EMBL; AK000302; BAA931068.1; -.
EMBL; AF001630; AAD00899.1; -.
EMBL; U61167; AAC50593.1; -.
HSSP; P29355; 1SEM.
Genew; HGNC:6184; ITSN2.
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Pfam; PF00036; efhand; 2.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00018; SH3; 5.
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InterPro; IPR000261; EPS15_homology.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
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2; PS50010; DH 2; 1.
3; PS50010; EF HAND; 1.
3; PS50001; EH; 2.
4; PS50003; EH DOMAIN; 1.
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                                   MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ
  IWALADMINDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG
                       MAQFPTAMNGGPNMWAITSEERTKHDRQFDNLKPSGGYITGDQARNFFLQSGLPAPVLAE
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V -> I (IN REF. 4).

R -> G (IN REF. 4).

R -> FAAAST (IN REF. 5).

KAVSPK -> FAAAST (IN REF. 6).

WEPKSYV -> EFAAAST (IN REF. 6).

GEKMPVQ -> VDAAANS (IN REF. 5).

GEKMPVQ -> VDAAANS (IN REF. 5).

K -> Q (IN REF. 2 AND 3).

Z 9 MW; 17B5C8629BBCFF9B CRC64;
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7; Mismatches 274;
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KKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYV
                                 SSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASN
                                                                                           GQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVAS--PAAKPAIPGEEFIAMYTY
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                                                                            GGRGWFPKSYVKIIPGSEVK-----REEPEALYAAVNKKPTSAAYSVGEEYIALYPY
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KKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHV 1111

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MEDLINE-99164083; PubMed=10064583;
Sengar A.S., Wang W., Bishay J., Cohen S., Egan S.E.;
Sengar A.S., Wang W., Bishay J., Cohen S., Egan S.E.;
                       InterPro;
InterPro;
                                                        EMBL; AF132479; AAD19747.1;
EMBL; AF132480; AAD19748.1;
HSSP; P29355; 1SEM.
MGD; MGI:1338049; Sh3d1B.
                                                                                                                                                 entities roor send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITSN2 OR SH3D1B OR E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Intersectin 2 (SH3 domain-containing protein 1B) (EH and SH3 domains protein 2) (EH domain and SH3 domain regulator of endocytosis 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Z0R6; Q9Z0R5;
28-FEB-2003 (Re
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                                                                                                                                                                                                                                                      dentate gyrus, ....
and in the amygdala.
SIMILARITY: Contains 2 C2 domains.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 1 EF-hand calcium-binding domain.
SIMILARITY: Contains 1 FH domain.
- SIMILARITY: Contains 5 SH3 domains.
- SIMILARITY: Contains 2 EH domains.
                                                                                                                                                                                                                                                                                                                                                                                             Name=2, Syponyms=Ese2, Short;
Name=2, Syponyms=Ese2, Short;
IsoId=Q9ZOR6-2; Sequence=VSD_003896, VSD_003897;
TISSUE SPECIFICITY: Widely expressed in adult tissues.
DEVELOPMENTAL STAGE: Widely distributed throughout the adult forebrain. Prominent expression was observed in the neocortex, the piriform cortex, the pyramidal cell layers of hippocampus, the piriform in several nuclei of the thalamus and hypothalamus
                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the endocytic process.
SUBCELLULAR LOCATION: Cytoplasmic
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May regulate the formation of clathrin-coated vesicles. SUBUNIT: Belongs to a complex that may contain multimers ITSN2 and Eps15, and different partners according to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) J. 18:1159-1171(1999).
FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1; Synonyms=Ese2L, Long;
IsoId=Q9Z0R6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                            non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGEINGVTGLFPSNYVKMTTDSDPSQQ 1191
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IPR000008; C2.
IPR002048; EF-hand.
IPR000261; EPS15_homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                 email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR ESE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1213
                                                                                                                                                               (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).
                                                                                                                                                                                            There are no restrictions in as its content is in
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Best Local S
Matches 658
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PRODOM; PD000066; SH3; 5.

SMART; SM00239; C2; 1.

SMART; SM00024; EFh; 2.

SMART; SM00027; EH; 2.

SMART; SM00027; EH; 2.

SMART; SM000236; RhoGEF; 1.

SMART; SM00236; SH3; 5.

PROSITE; PS50004; C2_DOMAIN_2; 1.

PROSITE; PS50001; DH 2; 1.

PROSITE; PS50001; EF_HAND; 1.

PROSITE; PS50001; EH; 2.

PROSITE; PS50001; EH; 2.

PROSITE; PS50001; DH 2; 1.

PROSITE; PS50001; DH 2; 1.

PROSITE; PS50001; DH DOMAIN; 1.

PROSITE; PS50001; DH DOMAIN; 1.

PROSITE; PS50002; SH3; 5.
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CONFLICT
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InterPro;
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290
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                                                                                                                                                                                                                                                               658;
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                                                                                                                                                                                                                                                                          Similarity
          DIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGMSVISSSSVD
                                                                                                        VIQPLPAFAHPAATWPKSSSFS--RSGPGSQLNTKLQKAQS-FDVASAPP---
                                                                                                                              ---SMPNLSIHOPLPPVAPIATPLSSATSGTSIPPLMMPAPLVPSVSTSSLP---
                                                                                                                                                 GIASMP-----PLTAVAPV---PMG-----SIPVVGMSPPLVSSVPPAAVPPLANGAPP
                                                                                                                                                                        IWALSDLNKDGKWDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGWG
                                                                                                                                                                                     IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG
                                                                                                                                                                                                                   MAQFFTAMNGGPNMWAITSEERTKHDKQFDNLKPSGGYITGDQARTFFLQSGLPAPVLAE
                                                                                                                                                                                                                                       MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ
                                      SPKTGTSEWAVPQPSRLKYRQKFNSLDKGMSGYLSGFQARNALLQSNLSQTQLATIWTLA
                                                     ----AAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLS
                                                                                   LIQPL-SIPYSSSTLPHASSYSLMMGGFG---GASIQKAQSLIDLGSSSSTSSTASLSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000219; RhoGEF.
IPR001452; SH3.
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IPR001849; PH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Coiled coil; Calcium-binding;
                                                                                                                                                                                                                                                              177;
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EF-HAND (POTENTIAL).
EH 2.
COILED COIL (POTENTIAL)
SH3 1.
SH3 2.
SH3 3.
SH3 4.
SH3 5.
                                                                                                                                                                                                                                                                                                          YABOTAL MAD 19748).

KQ -> NT (IN REF. 1; AAD 19748).

KQ -> (IN REF. 1; AAD 19748).
                                                                                                                                                                                                                                                             Score 3049.5; DB 1
Pred. No. 1.9e-109;
7; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                    DDLQLVIEVFQ
                                                                                                                                                                                                                                                                                                                                                              FTId=VSP_003896.
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN.
                                                                                                                                                                                                                                                                                                         G (IN REF. 1; AP
7050EFCC5F7983A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COIL (POTENTIAL)
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RESULT 7

EP15 - EP15

AC P425

DT 01-1

DT 15-4

DE EP16

DE EP16
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               protein)
EPS15 OR
                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Epidermal growth factor receptor substrate 15
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                                                Epidermal growth
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   (Human)
                                                                                                                                     STANDARD;
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/

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Matsuda M., Ota S., Tanimura R., Nakamu
Nagashima K., Kurata T.;
"Interaction between the amino-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enmon J.L., de Beer T., Overduin M.;
"Solution structure of Eps15's third I
Phe-Trp and Asn-Pro-Phe binding sites
Biochemistry 39:4309-4319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel gene, AF-1p, fused related to AF-4, AF-9 nor E Oncogene 9:1039-1045(1994).
                               + + + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98387926; PubMed=9721102;
de Beer T., Carter R.E., Lobel-Rice K.E.,
"Structure and Asn-Pro-Phe binding pocket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          natural target proteins.";
J. Biol. Chem. 271:14468-14472(1996)
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MEDLINE=94181254; PubMed=8134107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 281:1357-1360(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain.'
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rogue activator protein.
SIMILARITY: Contains 3 EH domains.
SIMILARITY: Contains 2 EF-hand calcium-binding domains.
SIMILARITY: Contains 2 ubiquitin-interacting motif (UIM) repeat.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/AF1pID11.html".
                                                                                                                                      TISSUE SPECIFICITY: Ubiquitously expressed.

PTM: Phosphorylation on Tyr-849 is involved in the internalization of Edr. Not required for membrane translocation after EGF treatment or for targeting to coated pits, but essential for a subsequent step in EGFR endocytosis (By similarity).

DISEASE: Involved in a t(1;11)(p32;q23) chromosomal translocation in acute leukemias causing fusion to the trithorax (MLL or HRX) gene product which contains DNA-binding motifs resulting in a
                                                                                                                                                                                                                                                                                                                                                                                             particular EGFR (By similarity)
SUBUNIT: Interacts with Stonin
binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the regulation of mitogenic signals and control of cell proliferation. Involved in the internalization of higand-inducible receptors of the receptor tyrosine kinase (RTK) type, in particular RGPB (BV 75-71-71-71).
                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic. Recruited to the membrane upon EGFR activation and localizes to coate
                                                                                                                                                                                                                                                                                                                                 similarity)
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GO; GO:0008283; P:cell proliferation; TA
GO; GO:0007173; P:EGF receptor signaling
GO; GO:0007048; P:oncogenesis; TAS.
InterPro; IPR002048; EF-hand.
InterPro; IPR002061; EFS15-homology.
InterPro; IPR000261; EFS15-homology.
InterPro; IPR000304; EFh; 3.
SMART; SM000726; EFh; 3.
SMART; SM000726; UIM; 3.
                                                                                                                                                                                                                                                                    CONFLICT
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L; Z29064; CAA823
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                                                                                                                    QVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPVPM
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   NTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL
                                                          GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL
                                                                                        RDEFAVAMFLVYCALE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocation;
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98673 MW;
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SH3-BINDING.
PHOSPHORYLATION
                                                                                                                                                                                                          Score 486.5; DE Pred. No. 4.7e-10; Mismatches 2
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                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
 SEQUENCE FROM N.A.
TISSUE=Fibroblast;
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                                                                                                                                                                                                                                                                                FSAYPS
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                                                                                                                                                                                                                                                                                                                                          PGKRSINKLDSPDPFKLNDPFQPFPGNDSPKEKDPEMFCDPFTSATTTTNKEADPSNFAN
                                                                                                                                                                                                                                                                                                                                                                                                   NEDPFRSATSSSVSNVVITKNVFEETSVKSEDEPPALP-
                                                                                                                                                                                                                                                                                                                                                                                                                             ---ELKGKTGWFPAN-----YAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP
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                                                                                                                                  growth
                                                                                                                             (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
rowth factor receptor substrate 15
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                                                                                                                                                                                                                                                                                 851
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                                                          Chordata;
Rodentia;
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                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00054; EFh; 4.

SMART; SM00027; EH; 3.

SMART; SM00726; UIM; 3.

PROSITE; PS00018; EF HAND; 2

PROSITE; PS50031; EH; 3.

PROSITE; PS50330; UIM; 2.
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                                                                                                                                                                                                             InterPro; IPR002048; EF-hand.
InterPro; IPR002261; EPS15_homology.
InterPro; IPR003903; UIM.
Pfam; PF00036; efhand; 4.
                                                                                                                                                                                                                                                                                                                      EMBL; L21768; AAA02912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                       between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20411232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION OF TYR-850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity.";
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Fazioli F., Minichiello L., Matoskova B.,
"eps15, a_novel tyrosine kinase substrate,
                                                                                                                                                                                                                                                           A54696; A54696.
; 1KYF; 12-JUN-02.
; 1KYU; 12-JUN-02.
; 1KYU; 11-SEP-02.
; MGI:104583; Eps15.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity). Interacts with Stonin 2.

SimcELLULAR LOCATION: Cytoplasmic Recruited to the plasma membrane upon EGFR activation and localizes to coated pits.

PTW: Phosphorylation on Tyr-850 is involved in the internalization of EGFR. Not required for membrane translocation after EGF treatment or for targeting to coated pits, but essential for a subsequent step in EGFR endocytosis.

SIMILARITY: Contains 3 EH domains.

SIMILARITY: Contains 2 EF-hand calcium-binding domains.

SIMILARITY: Contains 2 ubiquitin-interacting motif (UIM) repeats.
                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          particular EGFR.
SUBUNIT: Interacts with CRK via its SH3-binding sites
                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol.
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                                                       EF-HAND 1
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15 X 3 AA
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equired for ligand-regulated,
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                                                                                                                               3D-structure
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                                                                                                                                                                                                                                                                                                                                                                 Usage,
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                                                                                                                                                                                                                            QLQEVRKKCAEEAQLISSLK-----
                                                                                                                                                                                                                                             KLQDIRCRLATORQEIESTNKSRELRIABITHLQQQLQESQQMLGRLIPEKQILSDQLKQ
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SSNTSVETWKHNDPFAPGGTVVAAASDSATDPFASVFGNESFG-DGFADFSTLSKVNNED
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                    RALYPFESRSHDEITIOPGDIVMVDESQTGEP--GWLGGELKGKTGWFPANYAEKIPENE
                                          QSDPFVGSDPFKDDPFGKIDPFGGDPFKGSDPFASDCFFKQTSTDPFTTSSTDPFSASSN
                                                                                        PEIAPSDVTDESEAVTVAGNEKVTPR--FDDDKHSKEEDPFNVESSSLTDAVADTNLDFF
                                                                                                            ER-----DKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEA----EERAKPEMQDK
                                                                                                                                                                                                                                                                                                                   LOREK-----NNVEODLKEKE
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UIM 1.
UIM 2.
PHOSPHORYLATION (BY EGFR).
Y->F: INEFFICIENT EGFR INTERNALIZATION.
MW; 08AOCOD423F873C2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 486; DB 1;
Pred. No. 4.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVVSPAEKAKYDEIFLKTDKDMDGYVSGLEVRETFLKTGL
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EMBL; Z38062; CAA86208.1; -
EMBL; X79743; CAB38097.1; -
EMBL; M90688; AAA34841.1; -
PIR; S48440; S48440.
SGD; S0001445; PAN1.
                                                                                                                                                                                                                                                                                                                                                                                                                   LILLINGWORTH T., COMMOR R., Devlin K., Bankier A., Brown D.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87 (1997).
-i- FUNCTION: NOT KNOWN.
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P32521;
01-OCT-1993
                                                                                                                                             between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. Theis
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See )
or send an email to license@isb-sib.ch).
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MEDLINE=95282515; PubMed=7762303;
Manager J., Teodoru C., Valencia A., Sensen C., Wiemann S.,
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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SIMILARITY: Contains 2 EH domains.
CAUTION: WAS ORIGINALLY THOUGHT TO
POLY(A)-SPECIFIC RIBONUCLEASE.
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C., Zimmermann J., Sander C., Ar
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(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
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Query Match
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GO:0005866; C:plasma membrane; IDA.
GO:0008093; F:cytoskeletal adaptor activity; IPI.
GO:0007120; P:axial budding; IMP.
GO:0016288; P:cytokinesis; IMP.
GO:0006897; P:endocytosis; IMP.
GO:0006897; P:endocytosis; IMP.
GO:0007121; P:polar budding; IMP.
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Matches 261;

Local

Similarity

Pred. No.

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EMBL; X78214; CAA55048.1; -.
EMBL; X78214; CAA60797.1; -.
PIR; S45781; S45781.

GO; GO:0005857; C:actin cortical patch
GO; GO:0005857; C:bud neck; IDA.
GO; GO:0006897; C:bud tip; IDA.
GO; GO:0006897; P:endocytosis; IMP.
InterPro; IPR000261; EPS15_homology.
InterPro; IPR000449; UBA_domain.
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   "Scherens B., el Bakkoury M., Vierendeels F., Dubois B.,
"Sequencing and functional analysis of a 32,560 bp segi
left arm of yeast chromosome II. Identification of 26 c
frames, including the KIP1 and SEC17 genes.";
Yeast 9:1355-1371(1993).
-!- SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
-!- SIMILARITY: Contains 1 UBA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 150.8 kba protein in SEC17-QCR1 intergenic region.
YBL047C OR YBL0520 OR YBL0501.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95176707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of a 22.4 kb DNA fragment from the left chromosome II reveals homologues to bacterial proline murine alpha-adaptin, as well as a new permease and a
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SMART; SM00027; EH; 3.

SMART; SM00027; EH; 3.

SMART; SM00165; UBA; 1.

PROSITE; PS50031; UBA; 1.

PROSITE; PS50030; UBA; 1.

Hypothetical protein; Repeat.

DOMAIN 113 127

DOMAIN 135 227

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DOMAIN 138 386

DOMAIN 138 1380

SEQUENCE 1381 AA; 150783 MW.
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86; Conservative
                                                                               DOLKOVOONSIHRDSILTIKRALEAKELAROOLREQIDEVERETRSKLOEIDVFNNOIKE
                                                                                                     SKLNE----LTTDLQESQTKNAELKEQITNLNSMTASLQSQLNEKQQ-------
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                                LREIHSKQQLQKQRSLEAARLKQKEQE--RKSLEL---EKQKEDAQRRVQERDKQWLEHV 663
                                                                                                                                                   KLNNLRSTHDQNVKQTEQLEAQVL - - QVNKENE -
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                                                    GNSKAEPTKVATPSIPQQP-----
                                                                                      GTSKITPTEL--PKTAVQPAVCQVIGMYDYTAQNDD--ELAFSKGQIIN
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                                                                                                                                                             AQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSP
                                                                                                                                                                                                 -----ADSESEFENVANAGSMEQFETIDHKDLDDELQMNAFTGTLTSSSNPTI-PKPQV
                                                                                                                                                                                                                                   VIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSE-----GSGTAGKTGSLGKKPEI
                                                                                                                                                                                                                                                                        TEQVIKYPAPGTSPSHNEGNSKKASTNSILPVKDEFDDEFAGL-----EQAAVEEDNG-
                                                                                                                                                                                                                                                                                                        ---VRKSTSIDTGPTESPASIKRVASPAAKPAIP--GEEFIAMYTYESSEQGDLTFQQGD
                                                                                                                                                                                                                                                                                                                                            EFPPIQELHIDESDSSSSDDDE----FEDTRE----IPSATVKTLQTPYNAQPTSSLEIH
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                                                    ----IPLKNDPIVDASLSKGPIVN
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FIELZ M.J., ROGGER G.E.;

FIELZ M.J., ROGGER G.E.;

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES

-IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE

INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR

LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY

ISODIPEPTIDE BONDS. IT MAY SERVE AS SCARFFOLD PROTEIN, TOGETHER

WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN

ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLUCED IN

TYS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRHY RABIT P37709; 01-OCT-1994 01-OCT-1994 15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trichohyalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SUBUNIT: Homodimer (Probable).

TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES S
THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, S
THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE)
DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION C
THE EPIDERMIS.
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InterPro;

R InterPro; IPR002040,

R InterPro; IPR002040,

R Pfam; PP00036; efhand; 1.

DR Pfam; PP01023; S 100; 1.

DR ProDom; PD003407; CaBP_S100; 1.

DR PROSITE; PS000103; SITO CCBB; 1.

DR PROSITE; PS000103; SITO CCBB; 1.

DR PROSITE; PS000103; SITO CCBB; 1.

S-100 LIKE:

DOMAIN

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EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

The property of the property of
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02633; 4ICB.
InterPro; IPR001751; CaBP_S10
InterPro; IPR002048; EF-hand.
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PIM: SUBSTRATE OF TRANSCLUTAMINASE. SOME 200 ARGININES ARE PIM: SUBSTRATE OF TRANSCLUTAMINES BY PEPTIDYLARGININE DEIM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCILM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEFTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE WOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAIN 6 DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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L---KREDSVRKKEAEERAKPEMQ
                                                                                                                     LQREKRRQ-EREREYREEEKLQREEDEKRRRQEREROYRELEELRQEEQLRDRKLREEEQ
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29.7%;
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Pred. No. 3.1
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S-100
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute on the European Bioinformatics Institute on the content is in use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentifies requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION MEDILINE=9315897; PubMed=7686953; O'Keefe E.J., Hamilton E.H., Lee S.-C., Steinert P.M. "Trichohyalin: a structural protein of hair, tongue, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envelope precursor, and an intermediate linking) protein.";
J. Biol. Chem. 268:12164-1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermis."
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trichohyalin.
THH OR TRHY OR THL.
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                 EMBL; L09190;
                                                    entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93280194; PubMed=7685034;
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                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF THE EPIDERMIS.

THE EPIDERMIS.

DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOWAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROW STABILIZED BY JONIC INTERACTIONS. DOMAIN 6 1S THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOWAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Monomer (Probable).

TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH
THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND I
THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KLF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRAVULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIFEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANGOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN CITS ONN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                        DIFFERENT SPECIES.

PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                       SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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Pfam; PF01023; S 100; 1.
Pr0Dom; PD003407; CaBP S100
PROSITE; PS003018; EF HAND;
PROSITE; PS00303; S100_CABE
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InterPro; IPR002048; EF-hand.
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QERDROYR -> RSETGSTG (IN REF ^^
Q -> K (IN REF. 2)
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EF-HAND 2 (HIGH AFFINITY)
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P22793;
01-AUG-1991
                                                                                                                                                                                                                                                J. Cell Biol. 110:427-436(1990).

-:- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES.
-:- FUNCTION: INTERMEDIATE FILAMENTS (KIF) OF THI IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERWIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIFEFTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN
                                  <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                         Fietz M.J., Presland R.B., Rogers G.E., "The cDNA-deduced amino acid sequence for trichohyalin, differentiation marker in the hair follicle, contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Merino-Dorset horn X Border MEDLINE=90130632; PubMed=2298812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rietz M.J., McLaughlan C.J., Campbell M.T., "Analysis of the sheep trichohyalin gene: p calcium-binding roles of trichohyalin in th J. Cell Biol. 121:855-865(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=93260018; PubMed=7684041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trichohyalin.
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15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                            repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1016-1549 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae;
ISOId=P22793-2; Sequence=VSP_000847, VSP_000848; TISSUE SPECIFICITY: FOUND IN THE HARD EXERTINIZING TISSUES SUCH THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND I THE EPITHELIA OF THE TONGUE, HOOF AND RUMEN.

DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-SHIDDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRE ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF
                                                                                                                                                                                      SUBUNIT: Homodimer (PALTERNATIVE PRODUCTS:
                                                                                                            Name=Short;
                                                                                                                                           Name=Long;
                                                                                                                                                        Event=Alternative splicing; Named Comment=Additional isoforms seem
                                                                                                                                                                                                                      ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC DIFFERENTIATION.
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                                                                                                                         IsoId=P22793-1; Sequence=Displayed;
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m to exist;
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the hair follicle.
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                                                                                                                                                                                                                                     PROCESSING DURING TERMINAL
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Ptam; PP01023; S_100; 1.

ProDom; PD003407; CaBP S100; 1.

PROSITE; PS00018; EF HAND; 1.

PROSITE; PS00303; S100_CABP; FALSE_NEG.

Keratinization; Calcium-binding; Repeat; Citrullination;
Alternative splicing.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF hand.
Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z18361; CAA79165.1; -.
EMBL; X51695; CAA35992.1; -.
PIR; A40691; A40691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG DIFFERENT SPECIES.

PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 2 EF-hand calcium-binding domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
 986
1022
1045
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11099
11122
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11168
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11343
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413
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2-119.
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1-9.
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1-12.
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23 X.
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EF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
14 X 28 AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-100 LIKE.
                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                          AA APPROXIMATE TANDEM REPEATS.
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Matches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALD HUMAN STANDARD; PRT; 793 AA Q05682; Q13978; Q13979; Q14741; Q14742; Q1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Caldage (COM)
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VARSPLIC
                                    MEDLINE=92209999; PubMed=1555769;
Humphrey M.B., Herrera-Sosa H., G
"Cloning of cDNAs encoding human
Gene 112:197-204(1992).
                                                                                                                                                                                                                                   Novy R.E., Lin J.L.-C., Lin J.J.-C.; "Characterization of cDNA clones encoding a human fibroblast caldesmon isoform and analysis of caldesmon expression in no
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 4).
TISSUE=Lung fibroblast;
MEDLINE=91358497; PubMed=1885618;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caldesmon (CDM).
CALD1 OR CDM OR CAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
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SEQUENCE FROM N.A.
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                   transformed cell
                                                                                                                                                                                              Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chem. 266:16917-16924(1991).
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2-23.
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Missing (in isoform S /FTId=VSP 000848.
E -> G (IN REF. 2).
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EMBL; M83216; AAA58420.1; --
EMBL; M83216; AAA58419.1; --
EMBL; D90452; BAA14418.1; --
EMBL; D90453; BAA14419.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- DOMAIN: THE N-TERMINAL PART SEEMS TO BE A MYOSIN/CALMODULIN-BINDING DOMAIN, AND THE C-TERMINAL A TROPOMYOSIN/ACTIN/CALMODULIN-BINDING DOMAIN. THESE TWO DOMAINS ARE SEPARATED BY A CENTRAL HELICAL REGION IN THE SMOOTH-MUSCLE FORM.

-I- PTM: IN NON-MUSCLE CELLS, PHOSPHORYLATION BY CDC2 DURING MITOSIS CAUSES CALDESMON TO DISSOCIATE FROM MICROFILAMENTS.

PHOSPHORYLATION REDUCES CALDESMON BINDING TO ACTIN, MYOSIN, AND CALMODULIN AS WELL AS ITS INHIBITION OF ACTOMYOSIN ATPASE ACTIVITY. PHOSPHORYLATION ALSO OCCURS IN BOTH QUIESCENT AND DIVIDING SMOOTH MUSCLE CELLS WITH SIMILAR EFFECTS ON THE INTERACTION MITH ACTIN AND CALMODULIN AND ON MICROFILAMENTS REORGANIZATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                Genew; HGNC:14
GK; Q05682; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
   InterPro;
Pfam; PF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi E.-I., Kato I., Sobue K. "Genomic structure of the human ca
                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93101679;    PubMed=1465449;
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G. NATI. ACAD. SCI. U.S.A. 89:12122-12126(1992).

FUNCTION: ACTIN- AND MYOSIN INTERACTIONS IN SMOOTH MUSCLE AND MYOSIN INTERACTIONS IN SMOOTH MUSCLE AND NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN WHICH INCREASES THE STABILIZATION OF ACTIN FILAMENT STRUCTURE. IN MUSC TISSUES, INHIBITS THE ACTOMYOSIN ATPASE BY BINDING TO F-ACTIN. FILSUES, INHIBITS THE ACTOMYOSIN ATPASE BY BINDING TO F-ACTIN. THIS INHIBITION IS ATTENUATED BY CALCIUM-CALMODULIN AND IS POTENTIATED BY TROPOMYOSIN. INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN AND MITH CALMODULIN. ALSO PLAY AN ESSENTIAL ROLE DURING CELLULAR MITOSIS AND RECEPTOR CAPPING. SUBCELLULAR LOCATION: ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON
                                                                                      GO:0005856; C:cytoskeleton; TAS.
GO:0003779; F:actin binding activity; TAS.
GO:0005516; F:calmodulin binding activity; TAS.
GO:0005533; F:tropomyosin binding activity; TAS.
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                                                                                                                                                                                                                                                                                                                               D90452;
D90453;
JH0628; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q05682-3; Sequence=VSP_004154, VSP_004155; Name=4; Synonyms=WI-3B L-CAD II, 1-CAD; IsoId=Q05682-4; Sequence=VSP_004156; Name=5; Synonyms=HELA L-CAD II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1; Synonyms=H-CAD;
IsoId=Q05682-1; Sequence=Displayed;
Name=2; Synonyms=WI-38 L-CAD I;
IsoId=Q05682-2; Sequence=VSP 004155;
Name=3; Synonyms=HELA L-CAD I;
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      PF02029;
                                                                                                                                                                                                                                                                                               HGNC:1441;
IPR006017; Caldesmon.
IPR006018; Caldesmon_LSP.
2029; Caldesmon; 1.
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9:12122-12126(1992)
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FEKLKOKOOE-AALELEELKKKREERRKVLEEEEO--RRKOEEADRKLREEEEKRRLKEE
                                                                                                                                 ELEALNDKKHQLEGKLQDIRCRLATQRQEIES-----TNKSRELRIAEITHLQQQLQES
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                 AARLKQKEQERKSLELE--KQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKRE
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                                    VKSQNGEFMTHKLKHTENTFSRPGGRASVDTKEAEGAPQVEAGKRLEELRRRRGETESEE
                                                       SKLQEIDVFNNQLKELREIHSK-----
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375
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                                                                                                                                                                                                                                                                         108;
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                                                                                                                                                                                                                                                                                  Score 330; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLU.
POLY-ARG.
POLY-GLU.
POLY-GLU.
                                                                                                                                                      ERORIKEEEKRAAEERORARAEEEEKAKVEEOKRNKOLEE
                                                                                                                                                                                                                                                                                                                         Missing (In isoform /FTId=VSP 004156. V -> M (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRODOMYOSIN-BINDING (BY SIMILARITY).
STRONG ACTIN-BINDING (BY SIMILARITY).
CALMODULIN-BINDING (BY SIMILARITY).
WEAK ACTIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                              MDDFERRELARQKREEMALEAER -> MLGGSGSHGRRSL
AALSQ (in isoform 3 and isoform 5).
/FTIGE-VSP 004154.
Missing (In isoform 2 and isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CDC2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN AND CALMODULIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION
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MAK4 H

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DT 15-SEP

DC (MARHATA)

OX NCB1 T

RN [1] T

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RN I ISSUE

RY MEDLIN

RA YAO Z.

RT "A nov

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RA YAO Z.

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RT TACLIVA

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RT TISSUE

RA Wright

RA Salto

RA Submitt
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Micogen-activated protein kinase 4 (MEK kinase kinase 4)
(MEK kinase HGK) (Nck interacting kinase).
MAP4K4 OR HGK OR NIK OR KIAA0687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wright J.H., Wang X., Manning G., LaMere B.J., Le P. Khatry D., Flanagan P.M., Buckley S.D., Whyte D.B., Bischoff J.R., Lipson K.E., Jallal B., "The STE20 kinase HGK is broadly expressed in human can modulate callular transformation, invasion, and
  Submitted (APR-19
                                                                                                                                                                                                                                                      Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain woode for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Glioblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
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MEDLINE=99107863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12612079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                          "Isolation, expression profile and chromosome assignment
                                                                                                                                                                                           TISSUE=Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o 2., Zhou G., Wang X.S., Brown A., Diener K., Gan H., Tan T.-H.; novel human STB20-related protein kinase, HGK, that specifically tivates the c-Jun N-terminal kinase signaling pathway."; Biol. Chem. 274:2118-2125(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVRKKEAEERAKPEMOD-----KOSRLFHPHOEPAKLATOAPWSTTEKGPLTISAGES
                                                                                                                                                                                                               OF 262-1239 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                          OF 38-1239 FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKPAASDLPVPAEGVRNIKSMWEKGNVFSSPTAAGTPNKETAGLKVGVSSRINEWLTKTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VKVVYYRALY-PFESRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYA
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                                                                 Seki N., Hori T.;
                                                                                                                                                  oft A., Lauber (JAN-2000) to
  (APR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9890973;
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  gene.
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EMBL/GenBank/DDBJ databas
    EMBL/GenBank/DDBJ
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSAPAP-----
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B., Howlett
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(MEKKK 4)
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response to environmental stress and cytokines such as TNF-alpha.
Appears to act upstream of the c-jun N-terminal pathway.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- COPACTOR: Magnesium.
-!- SUBUNIT: Interacts with the SH3 domain of the adapter northine NCK (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a copyred the EMBL the Experiment of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=095819-5; Sequence=VSP_007054, VSP_007055, VSP_007056, VSP_007057, VSP_007058; TISSUE SPECIFICITY: Appears to be ubiquitous, expressed in all tissue types examined. Isoform 5 appears to be more abundant in the brain, isoform 4 is predominant in the liver, skeletal must be brain, isoform 4 is predominant in the liver, skeletal must be abundant in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 CNH domain.
CAUTION: Ref.4 sequence differs from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frameshift in position 1151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STE20 SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AF096300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ime=5; Synonyms=HGK-L;
IsoId=O95819-5; Seque
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Synonyms=HGK-S;
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InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00780; CNH; 1.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00036; CNH; 1.
SMART; SM00230; STKC; 1.
SMART; SM00219; TYCC; 1.
                                               NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                       GO; GO:0005524; F:ATP binding; IDA.
GO; GO:0004674; F:protein serine/threonine kinase; IDA
GO; GO:0006468; P:protein amino acid phosphorylation;
GO; GO:0007243; P:protein kinase cascade; IDA.
GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                              MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                    DOMAIN
                                                                                                                                           PROSITE; PS00107;
PROSITE; PS50011;
PROSITE; PS00108;
                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                      DOMAIN
                                                                                                                               ATP-binding;
                                                                                                                                                                                                                                                                                             InterPro; IPR001180;
                                                                                                                                                                                                                                                                                                                                                                                604666;
                                                                                                                                                                                                                                                                                                                                                                                                                      AB014587;
AL137755;
                                                                                                                                                                                                                                                                                                                                                                                                         AB013385; BAA33714.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                AY212247; AAO32626.1;
ABO14587; BAA31662.1;
                                                                                                                                                                                                                                                                                                                                                                                           HGNC:6866; MAP4K4
                                9 8pl
25
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289
14 1143
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                                                                                                                                           PROTEIN_KINASE_DOM;
PROTEIN_KINASE_ST;
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Missing (in isoto) isoform 5). /FTId=VSP_007054.
                                             ATP (BY SIMILAR ATP (BY SIMILAR BY SIMILARITY.
                                                                                     PROTEIN CNH.
                                                          7B)
                   (in isoform 5).
                                                           SIMILARITY).
                                                                                                     KINASE
                                                                                                                                                          kinase;
                                                                                                                                Transferase;
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                                  isoform
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	930	41 MWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTES-PASLKRVASDAA		유 왕
	940	9ATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQD : :: :: : : : : : : : : :	у 88 У 88	무장
	888	2 SSSN-EKPETDNWDTWAAOPSLTVPSAGQL	y 85 b 80	유 왕
	851	0 TDLTSAPAPKLALRETPAPLPVTSEEPSTTPNNWADFSSTWP	y 81 b 74	ੁਲ ਨ
	7 809	7 VDESQTG-EPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPV	y 767 b 681	₽ ₹
	1 766	2 WSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIOPGDIVM	y 722 b 625	ਲ ਝ
	721	9 KEAEERAKPEMQDKQSRLFHPH-QEPAKLATQAP	y 68	₽ ₹
	566	9 LKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRK	y 629 b 514	₽ ₹
	513	9 RALEAKELARQQLREQIDEVERETRSKIQEIDVFNNQLKELREIHSKQQIQKQRSLEAAR 	y 56	₽ ₹
	C 568	9 IESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQVQQNSLHRDSLLTLK 	y 509 b 479	₽ ₹
	508	9 ERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQE	y 449 b 433	₽ ₹
•	1 448) 432	1 ERKEREROEQEAKROLELEKQLEKORELERQREEERRKEIERREAAKRELERORQLEW :::	y 391 b 382	ਲ ਝ
	390	1 EEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERLAQLERAEQ	w w	~ ~
	39;	h 5.3%; Score 330; DB 1; Length 1239; Similarity 22.1%; Pred. No. 6e-06; 93; Conservative 116; Mismatches 222; Indels 342; Gaps	Query Match Best Local Matches 19	
		658 .658 839 839 1239 AA; 142100 M	T CONFLICT T CONFLICT CONFLICT SEQUENCE	0111
	-	/FTId=VSP_007057. C 1112 H -> HVRKNPHSM (in isof 5).	VARSPLI	444
		740 740	T VARSPLIC T	नेनेन
	ùκ	623 623	T VARSPLIC	4444
		C 569 622 Missing (in isoform 4 and isoform	T VARSPLIC	34

Search completed: December 4, 2003, 15:19:11 Job time : 22 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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sp_invertebrate:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length DB	B	ID
2 1	4264.5 4264.5	68.0	1220	13	Q8JFT5
ωĸ	1738.5	27.7	1014	ωF	OBINU2
4.	1735	27.7	1011	σ c	061639
տ	1702	27.1	1097	v	Q9VIF7
6	1698.5	27.1	1094	v	061618
7	1684	26.9	345	4.	QBIWH9
8	1530	24.4	611	4.	QBIWI5
9	1333	21.3	1097	υī	Q9U2T9
10	1314	21.0	755	11	Q8C4B5
11	1172	18.7	440		<u>0</u> 8C9C3
12	822.5	13.1	164		Q8CJ43
13	812.5	13.0	158		Q8CGU5
14	794.5	12.7	662	ഗ	Q8T068
15	704	11.2	276	11	Q8CD59
16	שאלע	B.6	864	4	00170

45	44	43	42 3			39	38					33	32	31	30			27	26 4							19	18	17
367	373	375	377.5	382	383.5	386	386	386	387.5	397	402.5	405	405	405	405	434.5	478	481	493.5	496.5	504.5	506.5	506.5	510.5	526.5	527	528	531
5.9	5.9	6.0	6.0	6.1	6.1	6.2	6.2	6.2	6.2	6.3	6.4	6.5	6.5	6.5	6.5	6.9	7.6	7.7	7.9	7.9	8.0	8.1	8.1	8.1	8.4	8.4	8.4	8.5
976	1596	1151	1129	1162	1909	2376	2376	1036	826	1089	1003	1480	1439	1148	944	1116	108	681	599	599	1106	796	751	819	1232	907	1253	1253
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Q9DUNO	Q8IJ44	Q9BX65	Q9QR71	Q98148	Q25893	Q966V1	Q9V5J0	Q9DUM3	Q9VPS3	040947	Q91LX9	Q18138	Q8MQC7	Q95ZY7	Q18137	Q9HGL2	Q8CJ62	Q8IFX4	Q91WH8	Q8CB60	Q8MMD3	Q9BIF4	Q23418	Q8CB70	Q8MMD2	Q60902	Q8WQ61	Q9W111
Q9dun0 kaposi's sa	Q8ij44 plasmodium	Q9bx65 homo sapien	Q9qr71 kaposi's sa	Q98148 kaposi's sa	Q25893 plasmodium		Q9v5j0 drosophila		Q9vps3 drosophila	O40947 kaposi's sa	ø			Q95zy7 caenorhabdi	Q18137 caenorhabdi	Q9hgl2 schizosacch	Q8cj62 mus musculu	Q8ifx4 caenorhabdi	Q91wh8 mus musculu		Q8mmd3 drosophila		Q23418 caenorhabdi	Q8cb70 mus musculu	Q8mmd2 drosophila	Q60902 mus musculu	Q8wq61 drosophila	Q9wlll drosophila

ALIGNMENTS

ō	SQ	E R	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	뮸	DR	DR	ვ	RĽ	RA	RР	RN	×	გ	8	8	သ	8	DE	B	Ţ	Ŋ	Dī	AC	IJ	RESULT Q8JFT5
Query Match 68.0%; Score 4264.5; DB 13; Length 1220;	SEQUENCE 1220 AA; 136351 MW; 1AB9134E2A4BA515 CRC64;	PROSITE; PS50002; SH3; 5.	PS50031;	, 胃	SMART; SM00326; SH3; 5.	SMART; SM00027; EH; 2	SMART; SM00054; EFh; 2.	•	PRINTS; PR00452; SH3DOMAIN.	PRINTS; PR00499; P67PHOX.	0036; efhand	IPR001452;	IPR000108; Neu_c	IPR000261;	InterPro; IPR002048; EF-hand.	CAD43427.1	AINS 5 SH3 DOMAINS.	Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.	Pandian R.;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=7955;		Teleostei;	-	Brachydanio rerio (Zebrafish) (Danio rerio).	SI:DZ173A8.1.	1)).	rotei	Last annotation	(TrEMBLrel. 22,	-2002 (TrEMBLrel. 22, Created)		Q8JFT5 PRELIMINARY; PRT; 1220 AA.	II. 1 기5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAQFFTEFGGGSDTWVISVDERAKHDQQFHSLTFTPAGFTTGDQARNFFLQSGLFAFILA
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TESPASLKRVASPAAKPA--
                                                                                               ASSSTTATPILPVSTEPASIAPPSSAPPPTGPASSSSSASSWADFSTTWPSNSAVEKQD
                                                                                                                                               VMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAP------
                                                                                                                                                                   KQWLEHVQQEEQP-----RPRKPHEEDRLKREDSVRKK---EAEERAKPEMQDKQS
                                                                                                                                                                                                                                        LEIDAFNTQLKELREIHNKQQRQKQKELE-ADITQPSHDRKSIDSQDSR------
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                          WRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGQRGWFPKSYVKLISGPVRKSMSIDSGS
                                     WRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGP
                                                             SDGWDAWPTQPTQPSLSVPSGGQIRQRSAFTPATLSGSSPSPVLGQGEKVEGLQAQALYP
                                                                      TDNWDTW----AAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYP
                                                                                                                                                                                                      ---LSGTDDGVSPAWRDDGLGKAPTPPVSQAWMSR----VREKKIVDAERHGFDQFCCCFM
                                                                                                                                                                                                                                                                                                                                                                                 FERGNLELEKRRQALLEQORKEQERLAALEKEEQERKERERLEQERRRQQELDKQLERQR
                                                                                                                                                                                                                                                                                                                                                                                            FERGSVELEKRRQALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEXQR
                                                                                                        -----APKLALRETPAPL-PVTSSEPSTTP-----NWADFSSTWPSSSN-EKPE
                                                                                                                                  VMVDESQTGEPGWLGGETKGKTGWFPANYAEKTPESEVPLSLRASAASSSAPKLGSHMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SIKLOKGOSVEAPSAPAAPPPADWAVSOSSRLKYROLFNSHDKWM
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8; Mismatches 184;
-IPGEEFIAMYTYESSEQGDLTFQQGDVIV
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 Query Match
Best Local
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SI:DZ173A8.1.
                            SEQUENCE
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              Pfam, PF00168; C2; 1.
Pfam, PF00036; efhand; 2.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SHJDOMATN
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Q8JFT4;

Q8JFT4;

Q8JFT4;

Q1-QT-2002 (TrEMBLrel. 22, Created)

Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)

Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

SI:GZ173A8.1.1 (Novel protein similar to intersectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 1 PH DOWAIN.
-!- SIMILARITY: CONTAINS 5 SH3 DOMAINS.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; AL606751; CAD43428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000008; C2.
InterPro; IPR002048; EF hand.
InterPro; IPR000261; EPS15_homolo;
InterPro; IPR000108; Neu_cyt_fact.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000219;
InterPro; IPR001452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTE--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTKKEGDWWTGTVSGKIGVFPSNYVKPKESEGLGSAGKTGSLGKKPEIAQVIAPYTATGA 1088
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AA;
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194115 MW;
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68.0**%**;

Score 4264.5; Pred. No. 2.3

4.5; DB 13; 2.3e-206;

Length

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LSGTDDGVSPAWRDDGLGKAPTPPVSQAWMSR---VREKKIVDAERHGFDQFCCCFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKL
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                                                                                                                                                                       TDNWDTW----AAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYP
                                                                                                                                                                                                                                                                                                                          VMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAP------
                                                                                                                                                                                                                                                                                                                                                                                                 RLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEIDVFNNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQKEDAQRRVQERD
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SDSPPSVKRPSPSLNKPTELGEGQNSNSNSMYPSKEYVAMYTYESNEQGDLTFQQGDVIT
                     WRAKKDNHLNFNKNDVITVLEQQDMWWFGEV
                                                                                                  WRAKKDNHLNENKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGFVRKSTSIDTGP
                                                                                                                                                 SDGWDAWPTQPTQPSLSVPSGGQIRQRSAFTPATLSGSSPSPVLGQGEKVEGLQAQALYP
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                                                                                                                                                                                                                                                           ----APKLALRETPAPL-PVTSSEPSTTP-----NNWADFSSTWPSSSN-EKPE
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                                                                          VQGQRGWFPKSYVKLISGP
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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Bardon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barli M.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Dodson K.Y., Dup L.E., Downes M., Duyann-Rocha S., Dunkov B.C.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugann-Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glana P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Stdarkiamos I., Simpson M., Stupski M.P., Smith T.,
RA Shue S.C., Stapleton M., Stupski M.P., Smith T.,
RA Shue S.C., Stapleton M., Stupski M.P., Smith T.,
RA Shue S.C., Stana M., Zhang G., Zhao Q. A., Ye J.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng L.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., 
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Q8INU2;
01-MAR-2003
01-MAR-2003
01-MAR-2003
CG1099-PB.
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Adams M.D., Celni
Amanatides P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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RA SEVANS C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers I., RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Busam D.A., RA Evans C.A., Center A., Champe M., Davenport L.B., Dietz S.M., RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., RA Carlson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D., RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Paragas V., Park S., Patel S., Pfeiffer B., Pholanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., "Sequencing of Drosophila melanogaster genome."; RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003669; AANI:
SEQUENCE 1014 AA;
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                                                               RENFERGSVELEKRROALLEOORKEOERLAQLERAEQERKERERQEOEAKROLELEKOLE
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1014 AA; 111890
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e EMBL/GenBank/DDBJ
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04; Mismatches
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O61639 PRELIMINARY; PRT; 1011 AA.

AC O61639;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-APR-2003 (TrEMBLrel. 23, Last annotation update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Dynamin associated protein isoform DAP160-2.

GN DAP160 OR CG1099.

GN DAP160 OR CG1099.

CS Drosophila melanogaster (Fruit fly).

CS Drosophila melanogaster (Fruit sequence)
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Eukaryota; Metazoa; Diptera; Brachycera; Muscomorpha;
CC Eukaryota; Metazoa; Diptera; Brachycera; Muscomorpha;
CN NCB1_TAXID=7227;
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STRAIN=OREGON N.A.
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SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 4.
PROSITE; PS00018; EF HAND; 2
PROSITE; PS50031; EH; 2.
PROSITE; PS50002; SH3; 4.
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InterPro; IPR002048; EF-hand.
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HSSP; P29354; IGRI
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InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., Salton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Pfeiffer B.D., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Pyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G., Andrews-Pfannkoch C., Baldwin D., RA Man K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., RA Burtis K.C., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., Davies P., Davi
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01-MAY-2000 (
01-MAY-2000 (
01-MAR-2003 (
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BERKELEY;
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DAP160 OR CG1099.
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.;
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.;
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhou Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhou Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhou X., Smith H.O.,
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Pfam; PF00038; SH3; 4.
PFINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 4.
SMART; SM00054; EFh; 2.
SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 4.
PROSITE; PS00018; EF HAND; 2.
PROSITE; PS00018; EF HAND; 2.
PROSITE; PS50001; EH; 2.
PROSITE; PS50002; SH3; 4.
Calcium; Calcium-binding; SH3 domain.
SEQUENCE 1097 AA; 120766 MW; 2573D7
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InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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                                                                                          LAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPG--TSKITPTELPKTA 1145
                                                                                                                                                                                LDTEVSQINTQSKTQSSEPAESYSRPMSRTSSMTPGMRAKRSEIAQVIAPYEATSTEQLS
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SSULT 6

O61618

O61618;

O61618;

O61618;

O1-AUG-1998 (TrEMBLrel. 07, Created)

O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)

O1-MRR-2003 (TrEMBLrel. 23, Last annotation update)

SUPNamin associated protein isoform DAP160-1.

AP160 OR CG1099.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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SMART; SM00027; EH; 2.
SMART; SM00026; SH3; 4.
PROSITE; PS00018; EF HAND; 2
PROSITE; PS50031; EH; 2.
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Pfam; PF00018; SH3; 4.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 4.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0023388; Dap160.
InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 SH3 DOMAINS.
EMBL; AF053957; AAC39138.1; -.
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HSSP; P29354; 1GRI
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                                                        NAKLLOLTQERAKWEAKSKASGAALGGENAQQEQ--
                                                                                                               NTQLNVELSTLNEKIKELSQRICDTRAGVTNVKTVIDGMRTQRDTSMSEMSQLKARIKEQ
                                                                                                                                            RKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQES
                                                                                                                                                                         RQREIEMEKEEQRKKELEAKEAARKELEKQRQQEWEQARIAEMMAQKEREQERVLKQKAH
                                                                                                                                                                                          KQRELERQREEERRKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKAR
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DKVENISKEIESKKEDININDVOMSELKAELSALITKCEDLYKEYDVORTSVLELKYNRK
                           EQLDEVERETRSKLQEIDVFNNQLKELRE----IHSKQQLQKQRSLEAARLKQKEQERK
                                                                                  QQMLGRLIPEK------QILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLR
                                                                                                                                                                                                                                   KENYVKGQAELDRRRKIMEDQQRKEREERERKEREEADKREKARLEAERKQQEELERQLQ
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                                                                                                                                                                                                                                                                                            SVSGVVSRPGSQPASRHASVSSQSGVGVVDADPTAGLPGQTSFEDKR
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                                                        LNAAFAHKQLIINQIK
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RESULT 7
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ID Q81W
AC Q81W
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AC Q81W
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Query Match
Best Local S
Matches 328
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Q8IWH9;
Q1-WAR-2003 (TrEMBLrel. 23, Created)
Q1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to intersectin 1 (SH3 domain protein) (Fragment).
                                                                                                                Strausberg R.;
Submitted (NOV-2002) to the
EMBL; BC039036; AAH39036.1;
NON TER 345 345
SEQUENCE 345 AA; 37077 MP
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                               FISSUE=Uterus;
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     328;
                                   Similarity
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37077 MW;
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  Score 1684; DB 4;
Pred. No. 2.5e-77;
5; Mismatches 10;
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O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ
EMBL; BC039963; AAH38963.1; -.
NON_TER 611 611
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Matches
                                                                                                                                            Query Match
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Q9U2T9;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00036; efhand; 2. Pfam; PF00018; SH3; 5. PRINTS; PR00452; SH3DOMAIN. ProDom; PD000066; SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McMurray A.A.;
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y116A8C.36 protein.
Y116A8C.36.
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                       SH3 domain.
                                                                                                                                                                                                                                        PROSITE; PS00152; ATPASE ALPHA_BETA; PROSITE; PS00018; EF HAND; 2. PROSITE; PS50031; EH; 2. PROSITE; PS50002; SH3; 5.
                                                                                                                                                                                                                                                                                                                                        SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002048; EF-h
InterPro; IPR000261; EPS1
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P29355; 1SEM.
WormPep; Y116A8C.36; CE23342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 5 SH3 DOMAINS EMBL; AL117204; CAB55138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000194; ATPase a/bcentre
InterPro; IPR002048; EF-hand.
InterPro; IPR000266; EF515_homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        none;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                               Local Sir
hes 369;
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<sub>5</sub>
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     WEVSDAEYQKNFAMF----
                                             WAITVEERAKHDQQFLSLKPIAGFITGDQ-----ARNFFFQSGLPQPVLAQIWALADM 67
                                                                                                                                                                                              1097 AA; 122072 MW;
                                                                                                 Conservative
                                                                                               21.3%; Sc
29.4%; Pi
tive 200;
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23,
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                                                                                               Score 1333; DE
Pred. No. 4.8e-
00; Mismatches
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Last annotation updat
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  ---GQLTGGQPFMDAVTARNALMRSNLPTQVLSQIWALSDL
                                                                                                                                                                                              1C2BA5F103968372 CRC64;
                                                                                                                          No. 4.8e-59;
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                                                                                                                                              DB 5;
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                                                                                                                                              Length 1097;
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                                                                                               234;
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182

SSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLT

AVAPVPMGSIPVVGMSPPLV-----SSVPPPAAVPPLANGAPPVIQPLPAFAHPAATWPK

----RHGSVDYSQTLPPAIDRRMSQSYIPSA--PVSIAGTP

NNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLT

DKDGRLDIREYSIAMRLALNCLAGIPIPPQLPPSLLVVPA--RNAPPTWPGS

SSRHNSISAGSPEN-----NDRNVFEGROLENWAIPHHNKLKYSOLFNALDKERLGSLS

196

142

197 242

ELV--

SQVGRSALGLSGLPTNVLAHIWFLSDVNKDGKLSVDEYAISQYMIEMFKSGFALPKITPL GPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPP

EXIPPSFRRVRSGSGMSVISSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGS

--RMCGISSRSANNTPELEPGAEPPQ--KSPAPKTFEDKRODNLSKGQ

421 303

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RESULT
QBC9C3
ID Q8
AC Q8
AC Q8
AC Q8
AC Q8
CO Q8
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Best Local (
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                                                              QBC9C3 PRELIMINARY; PRT;
QBC9C3;
QBC9C3;
Q1-MAR-2003 (TrEMBLrel. 23, Last se)
Q1-MAR-2003 (TrEMBLrel. 23, Last se)
Q1-MAR-2003 (TrEMBLrel. 23, Last an
SH3 domain protein 1B (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Crani
Mammalia; Eutheria; Rodentia; Sciur
NCBI TaxID=10090;
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Q8C4B5;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Pl
"Analysis of the mouse transcriptome based on
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL;. AK082606; BAC38546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1024 VTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAATGP
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ilarity 99.6%;
Conservative
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Rodentia;
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Last annotation updat
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Last annotation updat
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Pred. No. 2.7e-58;
                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                             PRT;
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PGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPA 1149
                             RCNGREGIFPANYVEISVQQAGDPTPPTQAPTPAAPPTVLCEAKVVVDFVASAPNQLGIK
                                                                                                                                                        KGDTIEVLEKQEMKWKGRNPAGEIGWFPKSYVKEVGATTSTTTPI-VSPSKASAGAPGAA
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                                                           TVGDKSGVFPSNYVRLKDSEGSGTAGKT--GSLGKKPEI---AQVIASYAATGPEQLTLA
                                                                                           AGAQYDVVPSDVTLQASETAPQQQLYTVIYDFEAVETTDLALHVGDTILVLEKNDEWWKG
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KEAEERAKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYP

----ADPFAQIAQAP--AHSKGAVDQSAFNIHDTYKCRALFA

-----LVHAQTHARSKIGEFEAKSAPASAAPAPAPAPAPTTTNGFPANFNDAFGEFD---K

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KEDAQRRVQERDKQWLEHVQQEEQPRPRKP----

-----HEEDRLKREDSVRK

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631

LELSTEKEKSYNQTEILKTNKEKYKTDVYSK-----LVAKREEYRNSFEL---

-EVERETRSKLQEIDVF-NNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQ LQETNQ----KTAIESQELGHQL---LQKQSAHKET-TQRKSELEALRRKRDAIRKAIEDAA

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LQESQQMLGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLD---ROOREKTLOFOLOALDEKVIDVEVDIGKAKEAVAEVTGFIERMRSTRDEKVARI----KE ABLERRRRVLEESEQRRRAEVEKKERESEAKKNRERQEKERQAEVERQAELERQRIISAQ VELEKRRQALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQRELERQ

RRKEIERR-----EAAKRELE-----RORQLEWERNRRQELLNORNKEQEGTVV

REEE--

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RESULT 12
Q8CJ43
ID Q8CJ4
AC Q8CJ4
AC Q8CJ4
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M3
DT 11-M3
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Query Match
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Q8CJ43;
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                                                           MBL; AF
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                           SEQUENCE
                                                                                                                                  transcripts.";
Ukr. Biokhim. Zh.
                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BALB/cxC57BLF1; TISSUE-Lung;
SKripkina I.Ya., Tsyba L.A., Slavov
"Novel splicing forms of human and m
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01-MAR-2003
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Nature 420:563-573(2002).
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the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
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                                           17677 MW;
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58; Mismatches
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RESULT 14
Q8T068
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QBCGUT 10
QBCGUT 01-M2
DT 01-M2
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Best Local Similarity
Matches 153; Conserv
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                                                                                 Q8T068;
Q8T068;
01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8CGU5;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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Drosophila melanogaster (Fruit i Eukaryota; Metazoa; Arthropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITSN.
                                          DAP160 OR CG1099.
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                                                                                                                                                                                                                                                                                                            RETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPET 860
                                                                                                                                                                                                                                                                                                                                                                        KGEWVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLAL
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(TrEMBLrel.
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation updatisoform 5 (Fragment).
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llarity 96.8%;
Conservative
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                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                Created)
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Pred. No. 7.1e-34;
0; Mismatches 0
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0; Mismatches
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  Hexapoda;
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Query Match
Best Local Similarity
Matches 221; Conser
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-- SIMILARITY: CONTAINS 4 SH3 DOMAINS.

EMBL, AY06517; AAL39662.1; --
FlyBase; FBgn0023388; Dag160.

InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 4.
ProDom; PD000066; SH3; 4.
SMART; SM00326; SH3; 4.
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                                         FPSNYVQKADVGTASTAAAEPVESLDQETTLNGNAAYTAAPVEAQEQVYQPLPVQEPSEQ
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      -SEGSG--
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01-MAR-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
SH3 domain protein 1B.
                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AKO31390; BAC27381.1; -
SEQUENCE 276 AA; 33547 MW; B8BC93085EDC2D7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

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Sequence 193, App
Sequence 195, App
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Sequence 31258, App
Sequence 39, App, Appl
Sequence 39, App, Appl
Sequence 30448, App
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Sequence 17146, Appl
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US-09-884-441-72

Sequence 72, Application US/09884441

Patent No. US20020119158A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121-462C7

CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

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; ORGANISM: Homo sapien
US-09-884-441-72
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                              121 GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180
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RESULT 2
US-09-907-969-72
; Sequence 72, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
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APPLICANT: Filing, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46268
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSEQ for Windows Version 4.0
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832 GAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCC 891	772 CAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAA 831 	712 GGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCT 771	652 CCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGT 711 	625 GCCCTCCAG	565 GGTCCAGGGTCACAATTAAACACTAAGTTACAGAAGGCACAATCATTCGATGTCGCCAGC 624	505 CTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCAAAGAGTTCTTCCTTC	445 TCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCT 504	401			01 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGG	241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300	181 ATATGGGCGTAGCGGACATGAATAACGATGGAAGGATCGATC	121 GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180	61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 120 	1 ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 60	Match 13.1%; Score 477.4; DB 11; Length 2017; ocal Similarity 55.5%; Pred. No. 8.6e-127; s 1111; Conservative 0; Mismatches 796; Indels 96; Gaps 6;	LENGTH: 2017 TYPE: DNA ORGANISM: Homo sapiens 09-907-969-72
Db &) B 4	§ § §	· B &	}	}) B &	B &	D Db	& B	Qy	B &	b b	? B 5	В В Х	G B 4	S B 5	DB QY	Db Qy
1995 AGATTAGAGCAAAAAAAAAAA 2017	1915 TTAGCCCTTGAACACTTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAA	1952 GAMAI IVAIGITII CAACAACCAGCIGAAGGAACIGAAGGAACIGGAAACAGGAA 1851 		AGITTUGGATAGAGCTUGGUTGACCCTCAAAGAGCCTTGGAAGCAAAGGAAGCAGCCTGGCCCTGATAGAGAGCTTGGAAGCAAAGGAGCTGGCCCTGATGAAAAGTCATCAGAAAAAGGAAGAATTA			1492 ATCAGGTGTCGACCCAGAGGCAAGAATTGAGAGCACGAACAAGTCTAGAGAG 1551		1455 AGTCAGAAGACCAGGGAACAAGAAGACATTGTCAGGCTGAGCTCCAGAAAGAA	1372 AATCAGAGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAAGG	1312 CGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACCGGAGACAGGAACTCCTG 1371	CTGGAGAGACAGCGGGAGGAAGAGAGAGAAGGAGATAGAAAGACGAGAGGCAGCAAAA		GAGGCTGAACGCAAAGCCCAGAAAGAGAAGAAGAGTGGGAAGCGGAAACAGAGAACTG	1132 CACANGGCAMAGAGGGAAAACCGCCCAAGGGCAGAGCAGCAGAGCGCAAA 1131	1012 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	952 TCCGTCATAAGCTCTTCTTGTGGATCAGAGGCTGCCTGAGGAGCGTCGTCAGAGGAT 1011 1051TTGATTCTGTTAATGGAACTCTGCCTTCATATCAGAAAACACAAGAA 1097	892 GTCCTGCCTCCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATG 951

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WESULT 3

US-09-827-271-72

Sequence 72, Application US/09827271

Publication No. US20030165504A1

GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6

CURRENT APPLICATION NUMBER: US/09/827,271

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

LENGTH: 2017

TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity 55.5%;
Matches 1111; Conservative
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Pred. No. 8.6e-127;
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APPLICANT: Bangur, Chaitanya S.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C9

CURRENT APPLICATION NUMBER: US/10/198,053

CURRENT FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 72

LENCTH: 2017

TYPE: DNA

ORGANISM: Homo sapiens

US-10-198-053-72
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; Publication No. US2003
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Publication No. US20030125246A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55
                                                                                                                      Query Match
Best Local Similarity
                                                                                                        Matches
                                                                                                                                                                                       OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (562)
OTHER INFORMATION: n e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZO7
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 568
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                               NAME/KEY: SITE LOCATION: (556)
                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (536)
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                         ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG
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                                     ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG
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                                                                                                        Conservative
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                                                                                                                          86.2%;
                                                                                                                                                                                          equals a,t,g, or
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                                                                                                        Score 356; DB 11;
Pred. No. 5.2e-92;
0; Mismatches 64
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US-09-879-957-193
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                                                                                                                                                                                         ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: CUnknown>
                                                                                                                      APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL,
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                     TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
       TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAY, Brian K.
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MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID
US-09-879-957-193
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 2873 bases
TYPE: nucleic acid
STRANDENNESS: single
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                                                                                                                                                                             AAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAA 3388
                                                                                                                                                                                                                                                                                                                           ANATTGCCCAGGTTATTGCTTCCTACGCTGCTACTGGTCCCGAACAACTCACCCTGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCCAAGCCAGCCATTCCCGGAGAGAGAGTTTATTGCCATGTACACATACGAGAGTTCTG
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TATGTCAGGTGATTGCTATGTATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCT
                        TGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCCTTCA
                                                                                                       AGGCCAGAGAAAAAAGCGACAGAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTGG
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Pred. No. 9e-
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NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 4210
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-868-125
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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                        CAGCCTATTCAGTT-----
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AGTGGTGGACAGGAAGTATTGGAGATAGAAGTGGAATTTTTCCATCAAACTATGTCAAAC
                             ACTGGTGGACGGAACGGTGGGCGACAAGTCCGGAGTCTTCCCTTCTAACTATGTGAGGC 3148
                                                                                                                                                                                                                                                                                                                                                        ATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTTGGGGAAGGTGCATGGAG
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Pred. No. 2.2e-84;
0; Mismatches 361;
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
PITTLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
SEQ ID NO 31258
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US-09-918-995-31258
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Publication No. US20030073623A1
                                                                                                          Query Match 8.9%;
Best Local Similarity 81.6%;
                                                                                               Matches
                                                                                                                                                                                                                              LENGTH: 503
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                    FEATURE:

FAATURE:

LOCATION: (1)...(503)

OTHER INFORMATION: n = A,T,C or G
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    CAAGTCAACAGTG
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                                                                                              Conservative
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                                                                                            Score 322.6; DB 11; Length Pred. No. 2.2e-82; O; Mismatches 84; Indels
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RESULT 9
US-09-879-957-39
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                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
ADDRESSEE: Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: USA
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                                                                  LENGTH: 747 bases
                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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KAY, Brian K.
FOWLKES, Dana M.
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTIVITE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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LENGTH: 270
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00664
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                                                                          GCTCCTTTGCCAGTGACCTCTTCTGAGCCCCTCCACAACCCCCCAACAACTGGGCAGACTTC
                                                                                                                                                                                  AAACCAGTGACCGATCTGACATCTGCCCCTGCCCCAAACTGGCTCTGCGTGAGACCCCT
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                                           GCCCCTTTGGCAGTAACCTCTTCAGAGCCCTCCACGACCCCTAATAACTGGGCCGACTTC
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87.2%;
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SSSED IN HELA, SIGNAL = 1.6

SSSED IN BRAIN, SIGNAL = 1.6

SSSED IN PLACENTA, SIGNAL = 1.6

SSSED IN PIACENTA, SIGNAL = 1.6

SSSED IN BOME MARROW, SIGNAL = 1.8

SSSED IN LUNG, SIGNAL = 3.2

SSSED IN LUNG, SIGNAL = 3.2

SSSED IN LUNG, SIGNAL = 2.7

SSSED IN ADULT LIVER, SIGNAL = 2.7

SSSED IN HEART, SIGNAL = 2.2

THAN HIT: AA773263.1, EVALUE 1.00e-112

SPROT HIT: Q15811, EVALUE 2.00e-45

T: gill526214, EVALUE 0.00e+00
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Pred. No. 9.8e-47;
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1.1

DB 9; 32;

Length Indels

270; 0;

Gaps

2538 180 2478 120 2418 60 2358 0

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RESULT 11
US-09-864-761-26948
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                                                                                                                                                                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 26948
LENGTH: 286
                                                                 OTHER INFORMATION: E
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CURRENT FILING DATE: 2001-05-23
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NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFULITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                OTHER
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FEATURE:
OTHER INFORMATION: MAP TO AP000311.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
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US20020048763A1
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                                                                   N: EXPRESSED IN BT474, SIGNAL = 0.87
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
N: EXPRESSED IN HBL100, SIGNAL = 1.3
N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
N: EXPRESSED IN LUNG, SIGNAL = 0.69
N: EXPRESSED IN PLACENTA, SIGNAL = 1.1
EXPRESSED IN A
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  BRAIN, SIGNAL = 0.69
PLACEMTA, SIGNAL = 1.1
HELA, SIGNAL = 0.92
ADULT LIVER, SIGNAL = 0.98
4488.1, EVALUE 0.00e+00
                                                                                                               FETAL LIVER, SIGNAL = LUNG, SIGNAL = 0.66
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
                                                                                                                                         APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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                              APPLICATION NUMBER: PCT/US01/00670
                                                FILING DATE: 2001-01-30
                                                                        APPLICATION NUMBER: PCT/US01/00661
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-26948
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                                                                                                                                                                                                       Sequence 30453, Application US/09864761 Patent No. US20020048763A1
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Best Local Similarity
                                                           APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                          FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                    INFORMATION:
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                                                                                                                       Rank, David R.
Hanzel, David K.
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                                                                                                                                                             , Sharron G.
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EST_HUMAN HIT: AA773263.1, EVALUE 1.00e-112
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine
SEQ ID NO 30453
LENGTH: 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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OTHER INFORMATION: EXPRESSE!
OTHER INFORMATION: MIT HIT: J
OTHER INFORMATION: EST HUMAL
OTHER INFORMATION: SWISSPROTON ASA 26.4.2.
               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/632,366 PRIOR PILING DATE: 2000-05-05-05 PRIOR PILING DATE: 2000-08-03
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                                                                                                                                                                                                                                             Rank, David R.
Hanzel, David K.
Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCCTTTGCCAGTGACCTCTTCTGAGCCCTCCACAACCCCCCAACAACTGGGCAGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGATGAAAGCCAAACTGGAGAACCCGGCTGGCTTGGAGGAGAATTAAAAGGAAAAGACA
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N: EXPRESSED IN HELA, SIGNAL = 1.2
N: EXPRESSED IN HELA, SIGNAL = 1.2
N: EXPRESSED IN BT474, SIGNAL = 0.76
N: EXPRESSED IN HBL100, SIGNAL = 1.5
N: EXPRESSED IN HELATO, SIGNAL = 1.5
N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
N: EXPRESSED IN ADULT LIVER, SIGNAL = 1
N: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
N: RITHIT: AF714487.1, EVALUE 0.00e+00
N: EST HOMAN HIT: AA773263.1, EVALUE 1.00e-112
ON: SWISSPROT HIT: Q15811, EVALUE 2.00e-45
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87.2%;
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Pred. No. 1e-46;
0; Mismatches
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SEQ ID NO 17146
LENGTH: 301
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OTHER INFORMATION: NOTHER INFORMATION
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-66-30
PRIOR APPLICATION NUMBER: US 09/774,203
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NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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ORGANISM: Homo sapiens
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DR FILING DATE: 2000-09-
DR APPLICATION NUMBER: F
DR FILING DATE: 2001-01-
DR FILING DATE: 2001-01-
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00669
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AACTGGAGAAGCAACTGGAAAAGCAGCGGGAGCTAGAACGGCAGAGAGGAGGAGGAGGA 240
                                                             AGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGAGAGGAGAGGA 1279
                                                                                                                              GGGCGGAGCAGGAGGAAGGAACGTGAGCGCCAGGAGCAAGAGCGCAAAAAGACAACTGG
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M: EXPRESSED IN HEART, SIGNAL = 2.2

M: EXPRESSED IN HBL100, SIGNAL = 3.2

M: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

M: EXPRESSED IN FLACENTA, SIGNAL = 2.3

M: EXPRESSED IN BRAIN, SIGNAL = 2.3

M: EXPRESSED IN BT474, SIGNAL = 2.2

M: EXPRESSED IN BOME MARROW, SIGNAL = 3.4

M: EXPRESSED IN HELA, SIGNAL = 3.7

M: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7

M: EXPRESSED IN LUNG, SIGNAL = 3.2

M: EXPRESSED IN LUNG, SIGNAL = 2.2

M: SWISSPROT HIT: O35601, EVALUE 3.50e-01

M: MISSPROT HIT: BEF4727 | EVALUE 3.60e-122
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82.3%;
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Pred. No. 1.2e-46;
0; Mismatches 49
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SEQ ID NO 17644
                                  OTHER INFORMATION: E OTHER INFORMATION: E
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PRIOR
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NUMBER OF SEQ ID NOS: 49117
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
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l, David K.
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IN HBL100, SIGNAL = 2.9
IN LUNG, SIGNAL = 3.2
IN HELA, SIGNAL = 3.2
IN FETAL LIVER, SIGNAL = 5.3
IN HEART, SIGNAL = 2.9
HIT: BE542917.1, EVALUE 3.00e-62
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APPLICATION NUMBER: PCT/US01/00662

FILING DATE: 2001-01-30

APPLICATION NUMBER: PCT/US01/00663

2001-01-30

APPLICATION NUMBER: PCT/US01/00670

2001-01-30

2001-01-30 NUMBER: PCT 2001-01-30

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; OTHER INFORMATION: SWISSPROT HIT: 035601, EVALUE 2.80e-01; OTHER INFORMATION: NT HIT: AF114487.1, EVALUE 1.00e-122 US-09-864-761-17644
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US-09-864-761-10314
                                                                                                                              PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
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Matches 222; Conserv
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PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-08
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/864,761
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Hanzel, David K.
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; OTHER INFORMATION:
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US-09-864-761-10314
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Best Local Similarity 81.6%;
Matches 222; Conservative
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SEQ ID NO 10314
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN BYA MARROW, SIGNAL = 0.87

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 32

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.66

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.92
                                                                                                                         2505 GCCCTCCACAACCCCCCAACAACTGGGCAGACT 2536
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ED IN FETAL LIVER, SIGNAL = 32
ED IN LONG, SIGNAL = 0.66
ED IN BRAIN, SIGNAL = 0.69
ED IN PLACENTA, SIGNAL = 1.1
ED IN HELA, SIGNAL = 0.92
ED IN ADULT LIVER, SIGNAL = 0.98
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Pred. No. 1.3e-44;
0; Mismatches 50
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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17313.032 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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ALIGNMENTS

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	RESULT 1 AF132478 LOCUS
Sengar, A.S., Wang, W., Bishay, J., Cohen, S. and Egan, S.E. The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Eps15	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3723)	Mus musculus (house mouse) Mus musculus	AF132478.1 GI:4378884	Mus musculus Esel protein mRNA, complete cds. AF132478	AF132478 3723 bp mRNA linear ROD 09-MAR-1999

Qy 559 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 618	Qy 499 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 558	OY 439 ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGAT	OY 379 GGTGATCAAGCGAGGAACTTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 438	Qy 319 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 378	259 ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 31	Query Match 73.2%; Score 3721.4; DB 10; Length 3723; Best Local Similarity 100.0%; Pred. No. 0; Matches 3722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	TTDMDPSQQ" BASE COUNT 1065 a 940 c 1026 g 692 t ORIGIN	WYTGTVGDKSGVFPSNYVELDSESGSTAGKTGSLGKKPELAQVGLFSYAATGPEQLTL APRQLTLILAKKNOGGAWKROGELQABGKKRQJGWFFDANYVKLLSPGTSKITJETELPKTAV QPAVCQVIGWYDYTAQNDDELAFSKGQIINVLNKEDPDWKKGEVSGQVGLFSONYVKL	KPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQAL YPWRAKKDNHLNINKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGFVRKSTSI DTGPTESPASLKRVASPAAKPAIPGEEFIAMYTYBSSEQGDLTFQQGDVIVVTKKDGD	EDSVRKKEAEERAKPEMODKOSKL-HEHDEDEAKLATOAPROTTEKGETZISAGESVKV VYYRALYPFESRSHDEITIOPGDIVMVDESOTGEPGWLGGELKGKTGWFPANYAEKIP ENEVPTPAKPVTDLTSAPAPKLALKETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNE	NRRQELLMORNKEØBGTVVLKARRKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQE IESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQVQQNSLHRDSLLT LKRALEAKELARQQLEQELDEVERETRSKLQEIDVENNQLKELREIHSKQQLQKQRSL EAABLKOKERETEKOKENARDSUNGEDKOKENDEENDEBEKHEFEDILFE	QSSRLKYRQLFNSHDKTMSGHLTGGQARTIIMQSSLLQAQLASIWNISDIDQDGKLTA EBETIAMHLIDVAMSGQDLPPULPBEYIPSFRKVRSGSGMSVISSSSVDQRLPBEBS SEDEQQPEKKLPVTFEDKKRENFBRGSVBLEKRRQALLEQQRKEQBRLAQLERABQER KRRENDKGDEAKROLFLEKOLGKERBREKERIFRERBAKKELFRORGLERABGER	/ L. TARIBA EL IONE MAQGEPTE FGGSLDVWAITVEERAKHDQQFLSLKFIAGFITGDQA / L. TARIBA EL IONE MAQGEPTE FGGSLDVWAITVEERAKHDQQFLSLKFIAGFITGDQA RNEF FFQSGLPQFVLAQIWALADWNNDGRWDQVEFSIAWKLIKLKLQGYQLFSTLPFVM KQQPVAISSAPAFGIGGIAGNEPLITAVAFVPMGSIFVVCKSSVEPAAVFPLANI CALBERTIONE DARAMBA DARBERTS CSGSGCOCOCOTO, TUTTUT VOX.QGEPUNG ABAR BENATUR	/cod/pro	/or /mc /db	2	2 (bases 1 to 3723) . 2 (bases 1 to 3723) . Sengar, A.S., Wang, W., Cohen, S., Bishay, J. and Direct Submission Submitted (02.MB-1000) Programs in Canada 6	JOURNAL EMBO J. 18 (5), 1159-1171 (1999) MEDLINE 99164083 DYTHMED 10044583
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3859 TATGTAAAGCTGACCACAGACATGGACCCCAGCCAGCAGTGAATCATATGTTGTCCATCC
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Sengar, A.S., Wang, W., Cohen, S., Bishay, J. and Egan,
Direct Submission
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The EH and SH3 domain Ese proteins
to dynamin and Eps15
EMBO J. 18 (5), 1159-1171 (1999)
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1 (bases 1 to 5145)
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                                        QPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKL
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DKYFSPKSNLQYKMYKTFIFLNEVLVKLPTDPSGDEPIFHISHIDRVYTLRAESINER
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WWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAATGPEQLTL
APGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAV
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPS
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/db_xref="GI:4378891"
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CHAPT 1448 a 1238 c 1415 g 984 t																			
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	219 AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG	CCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA	CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT	039 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC	ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT	19 TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAACTATGAGTGGACACTTA 97 	GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA 91	99 ANGAGITCTTCCTTCAGCAGAICTGGITCCAGGGTCACAATTAAACACTAAGTTACAGAAG 85 	GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA 79	GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC 73	19 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT 67	59 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 61 	99 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 55 	ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGAT	GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 43	GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 37	ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 31	ttch 71.6%; Score 3639.4; DB 10; Length 5145; sal Similarity 100.0%; Pred. No. 0; 3640; Conservative 0; Mismatches 1; Indels 0; Gaps	1448 a 1298 c 1415 g 984

3379 GGAGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGG	. dd	99 AAGAGGGAAGACAGTGTCAGGAAGAAGAAGGAGGCGGAAGAGAGAG	B &
3319 GTGATTGTGGTTACCAAGAAGATGGTGACTGGTGGACGGGAACGGTGGGCGACAAGTCC	Оу	2239 GAGCATGTGCAGGAGGAGGAGGAGGAGCCCCCGGAAACCCCACGAGGAG	용 성
001	- 4d	2179 TTAGAGAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTG 2238	B 8
		2119 CAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAAGAGCAGGAGAGAGA	g 99
3139 CTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCT 	ДУ	2059 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAG 2118	용 성
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3019 AAAGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAC 	рь	1939 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAG 1998 	용 성
	Db CS	1879 ATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCAT 1938 	ρ Q
) B &	1819 GCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTT 1878	용 성
581		1759 CGACTGGCAACCCAGAGGCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGCCTAAGAATT 1818 	유 성
779 521	. B &	1699 TTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGT 1758 	유 성
461	, B &	1639 AACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAAGACTCTGGAGTTTGAG 1698	유 왕
401	, B &	1579 GAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAGAGG 1638 	유
341	D CY	1519 CAGCGAGAGGAGGAGGAGGAAGGAAGTCGAGAGGCCGCGAGGCCGCAAAACGGGAACTG 1578	B 8
539 281	, pp &	1459 GAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGG 1518	8 8
221) B &	1399 CGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAGGAGGAAAAGAGCGGGAGCAGC	8 8
161) B 5	1339 AGTGTGGAGCTGGAGAAGCGCCCCCAAGCGCTCTTGGAGCAGCAGCAGCAGCAAGAGCAGGAG 1398	유 성
101	. da	1279 CCAGAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGAG	유양
0 2 3		961 AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG 1020	Дb

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1 (bases 1 to 5381)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-spilce cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J., Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                                                                                                             Submitted (16-DEC-1998) Medical and Molecular Genetics Center, Cancer Research Institute, L'Hospitalet de Llo., Avia. Castelldefels km. 2,7, Barcelona 08907, Spain Location/Qualifiers
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Pucharcos, C., Fuente
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kroytkalippesrshidiiiopenkolitureepempidesopp db_xref="GI:4808825"

Similarity Conservative 69.4%; Score 3529.4; Pred. No. 0; 0; Mismatches 0; 766; DB 9 Indels Length 5381; 69; Gaps

GGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCC GAGAAGAGTGGAGGCGCCAGGGGAAGGGAAGCGTAGCTTGGTTGCTCCGTAGTACGGCGGCT ACGTAATAGAACCATGGCTCAGTTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGC 305 GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCTGCGGCGCGCGTGAGCGGCACTGA GGGATGGTGTGCGCGGCTGCCGGACTCCGCCGTTCCTCGC-GCGGCTGCGGGCTGCACTGA CGCGAGGAAGAATCCCGAGCGGGCTCCGGGACG GAGGAGGAGTIGAGCGGCGCGGAGGGCGCAGCTTTGGTTTGCTTCCGTAGTTACGGCGGCT 66 CACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTTGG GGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTC CATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGC .AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC TTTGTGTGAGGGGCGGCCGCGCCCCGGAGATGAGGCGTCGATCAGCAAGGTGA GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC TTTGTCCCTGGGGCGGCAGCGGGACCCGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA -GACAGAGAGGCGGGCG 485 135 98 495 425 365 255 245 195 605 555 545 375 315

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2745 GCCAGTGACCTCTTCTGAGCCCTCCACAACCCCCAACAACTGGGCAGACTTCAGTTCCAC 2804	D Q	 1683 GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACT 1742
16 GACTG	DB 45	 1623 ACTCCTGAATCAGAGGAACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAA 1682
S CCCTGCAAACTATGCAGAAAAGATTCCAGAAAATGAGGTTCCACTCCACTCCAGCCAAACCAGT	Q & Q	1563 CGCAAAACGGGAACTGGAAAGGCAGCACACTTGAATGGGAACGGAACCGGAGACAGGA 1622
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36	Db	1443 GGAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCA 1502
76	Ωy	1383 GCGCAAAGAGCAGGAGCGGGTTGGCTCAGCTTGGAGCGCGCCGAGCAGGAGAGGAAGAGGAAGAGCG 1442
2400 TARGCTGGCCACCCAGGCACCCTGGTCTACCACAGAAAAAGGCCCGCTTACCATTTCTGC 2459	Db Qy	1323 GAACTTCGAGCGAGGCAGTGTGGAGCTCGAGAAGCGCCCCAAGCGCTCTTGGAGCAGCA 1382
56 56	Db Qy	 1266 GGATGAGCAGCAGCCAGAGAAAGAAACTGCCTGTGACATTTGAAGATAAGAAGAGGGGGA 1322
80 CCACC	Ωy	1206 GATGTCCGTCATAAGCTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGA 1265
23 GGAC 36 GGAC	Db Qy	 1146 GCCCGTCCTGCCTCCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGG 1205
163 GAGAAGAGCTGGAGTTAGAAAGAAGCAAAAGGAAGGCTCGAGAGACGAGTTCAGGAAAG 	Db QY	 1086 AGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCC 1145
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1983 GCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGAGGAGAGAGA	Qy db	 906 TGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTAT 965
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4942 TTTTAACTAGACTGIGGGGTTGCTACAGATTAATATGAAATGGGCTCCTGGTCCGTG 5001 [3885 CCCCAGCCAGCAATGAATCATATGTTGTCCATCCCCCCCTCAGGCTTGAAAGTCCTCAAA 3944 	~
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Query Match 69.2%; Score 3517.2; DB 10; Length 4025;	/codon_start=1 //prodon_start=1 //prodon_start=1 //prodon_start=1 //prodon_start=1 //protein_id="And SH3-domain containing protein EHSH1" //protein_id="And SH2-domain containing protein EHSH2-loop //protein_id="And SH2-domain containing cont	/or /mo /db 41.	JOURNAL Submitted (11-FEB-1999) Center for Basic Neuroscience and HHMI, Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235, USA FEATURES Location/Qualifiers source 1 4025	exocytosis and endocytosis? J. Biol. Chem. 274 (26), 18446-18454 (1999) 99303609 10373452 2 (bases 1 to 4025) Okamoto, M., Schoch, S. and Sudhof, T.C. Direct Submission		ACCESSION AF127798.1 GI:4835852 VERSION AF127798.1 GI:4835852 KEYWORDS SOURCE Rattus norvegicus (Norway rat) ORGANISM Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	AF127798 AF127798 AF127798 AF127798 AF127798 AF127798 AF127798 DEFINITION Rattus norvegicus EH- and SH3-domain containing protein EHSH1 mRNA,	 5106 TCTCAATAAAAAT	Qy 5002 TGTGTGTTAACTTGTGCTGTAGCTGAAGCCGTGTGTCCTTAGATATTAGTTGGAAGT 5058
Qy	819 ATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAGGCACAATCATTCGATGTCGC (Qy 759 GCCTCTGCCTTGCGCATCCTGCAGCCACATGGCCAAAGAGTTCTTCCTTC	QY 699 ATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACA 758	Oy 579 GGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATTGCTAGCATGCACCACTCAC 638	519 GAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGT 	Qy 399 TITTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACAT 458	QY 339 GCAGTTCCTTAGCCTGAAGCCGATAAGCGGATTATTACTGGTGATCAAGCGAGGAACTT 398	279 TTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCA 	Best Local Similarity 93.4%; Pred. No. 0; Matches 3734; Conservative 0; Mismatches 243; Indels 21; Gaps 5; Oy 219 GAGATGAGGGTCGATCAGGAAGGTGAACGATAGAACCATGGCTCAGTTTCCGACACC 278

2019 GGTGGAGAGCAGGAACCAGGAACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	659 CGTGGTCCTGAAGGCAAGGAGAGACTCTGGAGTTTGAAGTTAGAAGCTCTGAATGACAA 1	1021 GCGGCTGCCCGAGGAGCCATCGTCAGAGGATGAGCAGCTAGGAGAAAAGAAGAAGCTGCCTGT 1080 1299 GACATTTGAAGATAAGAAGCGGGAGAACTTCCAGGCGAGCAGCTGGAGAAGCAGCTGCCTGT 1080 1081 GACATTTGAAGATAAGAAAGCGGGAGAACTTCCAGAGCGAGC
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Antonarakis,S.E.
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Direct Submission
Submitted (05-MAY-1998)
Michel-Servet, Geneva 4
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                                                                                                 AGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGG
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                    TGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTT 344
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Db 2293 AGTCCACTTACCATTCTGCACAGGAAAATGTAAAAGTGGTGTATTACCGGGCACTGTA 2352 Qy 2499 CCCCTTTGAATCCAGAAGTCACGATGAGATCACCATCCAGCGAGGAGATATAGTCAT 2555	OY 23.79 CCATCUCKATCAGGAGCAGCTGGCCCAGCCAGCCCTGTACACAGAAAA 2438 Db 2233 CCATCAACACCAAGAACCAGCTAAGCCAGCTGTCCAGGCACCAGGCAGCAGAAAA 2292 OY 2439 AGGCCCGCTTACCATTTCTGCACAGGAGAGTGTAAAAAGTGGTATATTACCGAGCGCTGTA 2498	2319 GAAGAAGGAGGCGGAAGAGAGACCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTTTT	Qy 2259 GCAGCCACGCCCCCGGAAACCCCACGAGGAGACAGACTGAAGAGGGAAGACAGTGTCAG 2318	Qy 2202 TCAGAGACGAGTTCAGGAAAAGGGACAATGCGATGGAGCATGTGCAGCAGGAGGA 2258	Qy 2142 ACTGAAGCAGAAAGAGCAGGAGGAGGAGAGAGACCTTGGAGTTAGAGAAGCAAAAGGAAGACGC 2201	OY 2082 ACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCAGCGCG 2141 D	Qy 2022 GGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACCAGCTGAAGGA 2081	OY 1962 ANGAGCCTTGGANGCANAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGACGAT 2021	Qy 1902 TGACCAGTTAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCAA 1961	QY 1842 GCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAG 1901	QY 1782 AATTGAGAGCACGAACAAGTCTAGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCA 1841	Qy 1722 GCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCCAGAGGCAAGA 1781	Qy 1662 GGTCCTGAAGGCAAGAGACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAA 1721	Qy 1602 GGAACGGAACCGGAGACACGAATCAGAGGAACAAGGAGCAGGAGGACGGCACCGT 1661	QY 1542 GGAGATCGAGAGGCGGGAGGCCGCAAAACGGGAACTTGAAATG 1601	Qy 1482 GGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGAGCAGCAGCAGAGAGAAGGAGAAGAAGAAGAAGA	Qy 1422 CGAGCÀGGAAGGAAGAGGAAGCAGGAGCAGCAGGAGCAGGAGCT 1481

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Okamoto, M., Schoch, S. and Sudhof, T.C.
EHSH1/intersectin, a protein that contains EH binds to dynamin and SNAP-25. A protein connec excytosis and endocytosis?
J. Biol. Chem. 274 (26), 18446-18454 (1999) 99303609
                                                                                                                                                                                                                  Okamoto,M., Schoch,S. and Sudhof,T.C.
Direct Submission
Submitted (02-MAR-1999) Center for Basic Neuroscience and HHMI,
Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX
                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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IESTINKSRELRIAEITHLOQULQESQQMLGRLPERGRULSDQLKQVQQNSLHRDSLLT
LKRALEAKELARQLREGLDEVEKETRSKLQEIDVFNNQLKELREIHSKQQLQKQRSI
EAERLKQKEGGERKSILELEKQKEEGGRRVQERDKQMPBTTEKGPLTISAQESAKVV
YYRALYPESRSHDEITIQPDIVMVKGEWDDSSQTEPGRTGMFPANYA
EKIPENEIPTPAKEVTDLTSAPAFKLALKETPAFLFVTSSEPSTTENWADEPSTWPS
STNEKPETDNWDTWAAQPSLTVBSAGGLRQRSAFTPATATGSSEPVLGGGEKVECLQ
AQALYPMRAKKDNILNENKSDVITVLEQGDENGMFPESQCKWFPKSTERFSTENWADEPSCTWFS
KKNPGGWWEGELQARGKKRQIGWFPANYVKLLSFGTSKITFTELFKTAVQPAVCQVIG
MYDYTAQNDDELAFSKGQIINVLSKEDPDWWKGEVGGVGLFPSNYVKLTSGPVK
STSIDTGPTEAPSSLKRVASPAKKR

Best Local Similarity Matches 3535; Conserv GAGATGAGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACC GCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTT GTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTAACAGGTCCCCAGGCAAGAAC CAGCGCCCCTGCAGCGGCAGAATGGGCTGTGCCTCAGTCGTCAAGACTGAAATACAGGCA ATCTTCTGTCCCTCAAGCAGCAGCAGTGCCTCCCTGGCTAACGGGGCCCCTCCTGTCATACA ATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACA GGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATTGCTAGCATGCCACCACCACTCAC GAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCCTGTCATGAAACAGCAACCAGT GAATAAGGACGGAAGGATCAGGTGGAGTTTTCCATAGCCATGAAGCTCATCAAACT GAATAACGATGGAAGGATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACT TTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACAT TTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAAGGGCCAAGCATGACCA GAGATGAGGCGTCGATTAGCAAGGTAAAGGTAACAGAACCATGGCTCAGTTTCCGACACC CAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCAATGCTGAAATACAGGCA ATCTGGTCCAGGGTCACAATTAAACACTAAACTACAGAAGGCACAATCATTTGATGTAGC ATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAGGCACAATCATTCGATGTCGC AGCIGTIGCIGCIGIGCCAAIGGGCICCAITCCAGIIGTIGGAAIGICICCACCCITAGI GGCCATCTCTAGTGCACCAGCGTTTGGTATAGGAGGGATGGCTGGAATGCCACCACTGAC TTTTGGTGGGAGCCTGGACATCTGGGCCATAACCGTGGAGGAAAGAGCCAAGCATGACCA AGCTGTTGCTCCCGTGCCAATGGGCTCCATCCCAGTTGTTGGAATGTCTCCGCCCTTAGT 1088 Conservative Ø 972 61.0%; a 1058 0; Score 3103.6; Pred. No. 0; Mismatches ω 694 В 229; 10; Indels 234; Length Gaps 338 638 578 120 720 660 600 818 540 758 480 869 420 360 300 518 240 458 180 398 60 278 998 9

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                      GGGGCTTTCCTAGTCACTCAGACTGACCGGCCCCGCCT
                                                                                                                  AGTCACTGCGTGCAGAGGCAGAAGCAAATTGCAGAACTGCACAGGGTGGTGGGTCCTTTT
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-GTGCTTTCCTAGTCACTCAGACTGACGGCCCCGCCTT
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1 (bases 1 to 6439)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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Pucharcos, C., Fuentes, J.J., Pritchard, M. and Estivill, X.
Direct Submission
Submitted (16-DEC-1998) Medical and Molecular Genetics Center,
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FSPDDFLGRTEIRVADIKKDQGSKGPVTKCLLLHEVPTGEIVVRLDLQLFDEP
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Oy 906 TGTGCCTCAC 1	846 1-1	786 AGC	726 TC	Qy 666 CATTCCAGT: Db 676 CATTCCAGT:	Qy 606 TATAGGAGG	Qy 546 CACACTTCCC Db 556 TGCACTTCCC	Qy 486 GGAATTTTCO	Qy 426 TGTCTTAGCA Db 436 TGTTTTAGCA	Qy 366 GGGATTTATT Db 376 TGGATTCATT	Qy 306 CATAACTGTO Db 316 CATAACTGTO	Qy 246 ACGTAATAGJ Db 256 AAGTAACAGJ	Qy 186 TTTGTGTGAG Db 196 TTTGTCCCTG	Qy 127 GGGATGGTG: Db 136 GGGATGGTGT	Qy 67 CGCAAGGGA Db 87 CGCGAGGAA	Qy 7 GAGGAGGAG Db 27 GAGAAGAGTY	Query Match Best Local Similarity Matches 3367; Conserva
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. 1 1 9 9	0—0 C	a—a a	TGCGCATCCTGC 7	CTGTCCCTCCAGCAGCAGTGCC 7	IGTTGCTCCTGTGCCAATGGGCTC 6	TTTGG 6	CTACAAGGATATCAGCTCCCCTC 5	2—2 4 4	CTTTTTTTCCAATCTGGGTTACCTCAGCC 4:	ი — ი	ი—ი ა	NN	CTGA 1	დ— დ 1-	о о н—н	9; Length 6439; 515; Indels 33; Gaps
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1996 ACTACCAGAAGCAGCAGCAGGGCCCCTGGAGGGAGCAGCTGAAAGAAA	1923 GCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGA	1863 AATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCA 	1803 TAGAGAGCTIAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCA 1862 	1743 TCAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAAATTGAGAGCACGAACAAGTC	1683 GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACT 	1623 ACTOCTIGAATICAGAGGAACAAGAGGAGGACGTGGTTCCTIGAAGGCAAGGAGGAAG 1682	1563 CGCAAAACGGAAACTGGAAAGGCAACTGGAACGGAACCGGAACCGGAACACGGAACACGGAACACGGAACACGGAACACGGAACACGGAACACGGAACACGGAACACGGAACACGGAACACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACTGAAGGCAACGAACTTGAAGGCAACGGAATCGAAGGCAAGA 1635	. 1503 GCGGGAGCTGGAGCGGCAGCGAAGGAGAGAAGAAGAGAAGCAGACCGCGAAGGC 	1443 GAGCGCCAGGAGCAGAGCCCAAGCGGCAGCTGGAGCTGGAGAACCAGCTGGAGAAGCA 	1383 GCGCAAAGAGCAGGAGCGGTTGGGTCGAGCTGGAGCGCCGAGCAGGAGAGAAGAGCGGTTGGAGGAGAGAGGGGGGGG	1323 GAACTTCGAACGAGGCAGTGTGGAGCTGGAGCAGCGCCCAAGGCGCTCTTGGAGCAGCAGCA	1266 GATICHGCHGCHGCHGCHGCHGIGACHTTIGANGHTANGAGCGGGA	1206 GAIGICGICATAAGCICTICTICTICTIGGAICAGAGCIGCIGAGAGCCGICGICAGA 1265 1216 TATATCTGTCATAAGCTCAACATCTGTAGATCAGAGGCTACCAGAGGAACCAGTTTTAGA 1275	1146 GCCGTCCTGCCTCCAGAATACATCCCTTCCTTCCTCCAGAAGAGTTCGCTCCGGCAGTGG	1086 AGAACAATTTATCCTAGCTATGCCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCC	1026 GGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGC 1085

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.4 AF064244 7247 bp mRNA linear PRI 21-NOV-1998	3916 CCCAAGCCAATG 3930	3885 CCCCAGCCAGCATG 3899	3856 AGTCAATGGACAAGTGGGGCTCTTCCCATCCAATTATGTGAAGCTGACCACAGACATGGA 3915	3825 AGTCAGTGGGCAAGTTGGGCTCTTCCCAATCAATTATGTAAAGCTGACCACAGACATGGA 3884	3796 CAACAAGGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGAAAAGGAGA 3855	3765 CAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAGA 3824	3736 AGTGTGCCAGGTGATTGGGATGTACGACTACACCGCGCAGAATGACGATGAGGTGAGCTTT 3795	3705 AGTGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCCTT 3764	3676 AAGCCCTGGGACGAAGAATCACTCCAACAGAGCCACCTAAGTCAACAGCATTAGCGGC 3735	3645 AAGCCCCGGAACAAGCAAAAATCACCCCAACTGAGCTACCCCAAGACCGCCAGTGCAGCCAGC	3616 GCAAGCACGTGGGAAAAAGCGCCAGATAGGCTGGTTCCCAGCTAATTATGTAAAGCTTCT 3675	3585 GCAAGCTCGAGGGAAAAAGCGGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCT 3644	3556 CCCTGGTCAGCTGATTTTGATCCGAAAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAGGCT 3615	3525 TCCTGGGCAGCTGATTCTGATCCGGAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAACT 3584	3496 TGAAATTGCCCAGGTTATTGCCTCATACACCGCCACCGGCCCCGAGCAGCAGCTCACTCTCGC 3555	3465 TGAAATTGCCCAGGTTATTGCTTACGCTGCTGCTGGTCCCGAACAACTCACCCTGGC 3524	3436 GCTTAAAGATTCAGAGGGCTCTGGAAACTGCTGGGAAAACAGGGAGTTTAGGAAAAAAAA	3405 GCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGGAAAAACAGGGAGTTTAGGAAAAAAAA	3376 TGACTGGTGGACAGGAACAGTGGGCGGACAAGGCCGGAGTCTTCCCCTTCTAACTATGTGAG 3435	3345 TGACTGGTGGACGGGAACGGTGGGCGACAAGTCCGGAGTCTTCCCTTCTAACTATGTGAG 3404	3316 TGAGCAAGGAGATTTAACCTTTCAGCAAGGGGATGTGATTTTGGTTACCAAGAAAGA	3285 TGAGCAAGGAGATTTAACCTTTCAGCAAGGGGATGTGATTGTGGTTACCAAGAAAGA	3256 AGCAGCCAAGCCGGTCGTTTCGGGAGAAGAATTTATTGCCATGTACACTTACGAGAGTTC 3315	3225 GGCCGCCAAGCCATTCCCGGAGAAGAGAGTTTATTGCCATGTACACATACGAGAGTTC 3284	3196 TACAAGCATGGATTCTGGTTCTTCAGAGAGTCCTGCTAGTCTAAAGCGAGTAGCCTCTCC 3255

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165 GCGGCGTGCGGCTGCACTGATTTGTGTGAGGGGGGGCGCGCGC	D Qy	TITLE Direct Submission JOURNAL Submitted (05-MAY-1998) Genetics and Microbiology, CMU, 1 rue Michel-Servet, Geneva 4 CH-1211, Switzerland Location/Qualifiers Source 1, 7247	_

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- 2γ	dg VQ	B 8	B &	B &	Db Oy	9d Qv	4g 4g	B &	D Q	υb	Qγ	Db Qy	Db Qy	g dg	B 8	S & &	Оу Db	Db
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SOURCE
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                                                                                                                                                                                                                                                                                                          University Ave, Madison, WI Location/Qualifiers
                                                                                                                                                                                                           Submitted (30-OCT-1997) Pharmacology, University Ave, Madison, WI 53706-1532,
                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Xenopus laevis intersectin mRNA,
                                                                                                                                                                                                                                                         2 (bases 1 to 4103)
Hoffman, N.G., Hardison, N.L., Yamabhai, M. and Kay, B.K.
                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
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/function="involved in endocytosis"
/note="EH domain and SH3 domain containing protein;
/note="EH domain and SH3 domain containing protein;
similar to intersectin binding proteins Ibp1, encoded GenBank Accession Number AF057285, and Ibp2, encoded I GenBank Accession Number AF057286, and mouse
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AUTHORS
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Best Local Similarity 85.9
Matches 1832; Conservative
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HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)
PN JP 2002017375-A/2599
PD 22-JAN-2002
PD 22-JAN-2002
PD 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAMA,TAKAO ISOGAI,KOJI IPI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIIO
                     344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10,
PC C12
Primer
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1 (Dases 1 to 2131)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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JP 2002017375-A/2599.
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TCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTT
                                                                             GTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGT
                                                                                                                                         GAGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTTCCCACACCTTTCG
                                                                                                                                                                                                          GTTGCTCCGTAGTACGGCGGCTCGCAAGGGAGCATCCCGAGCGGGCTCCGGGACGGCCGG
                                                      GTGGCAGCCTGGATATCTGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGT
                                                                                                                      GAGGCGTCGATTAGCAAGGTAAAAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTG
                                                                                                                                                                                       AGCGGCGCGTGAGCGGCACTGATTTGTCCCTGGGGCGGCAGCGCGGGACCCCGGCAGAT
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mer for synthesizing full-length cDNA and use thereof FH R
Location/Qualifiers
CDS (205) (2130)
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
469 c 526 g 44
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GCCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGGGGCAAGCAGCTCTCCTGGAACAGCAGCGCAAGGAGCAGGAGCGCCTGGCCCAGCTGGAGCGGG
                                                                                                                                      CATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCC
                                                                                                                                                                                               TGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGC---CAGAGAAAGAAACTGCCTGTGA
                                                                                                                                                                                                                                                         GAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGC
                                                                                                                                                                                                                                                                                                                      TTATGCAGTCAAGTTTACCACAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTG
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REFERENCE AUTHORS

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TITLE JOURNAL REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 11 AK074554 LOCUS DEFINITION 2131 bp Homo sapiens cDNA FLJ90073 fis, cl to Homo sapiens intersectin short AK074554 Unpublished
2 (bases 1 to 2131)
Isogai, T. and Otsuki, T. Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suguki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,X., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and AK074554.1 GI:22760070 oligo capping; fis (full Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; NEDO human cDNA sequencing Ninomiya, K. Chordata; Primates; insert project Craniata; Vertebrata; Catarrhini; Hominidae; mRNA linear clone HEMBA1004110, rt form mRNA. sequence) Euteleostomi; PRI 03-SEP-2002 highly similar

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/04 CIBICCLICHAGCHAGIACLICCCCIAGCIANCAGGGCICCICCCAIALHAGCCIC /63		44 TTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTT	584 TTTCCAGTGCACCAGCATTTGGTATAGGAGGGATTGCTAGCATGCCACCACCACAGCTG 643	524 TACAAGGATATCAGCTCCCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTA 583	464 ACGATGGAAGGATGAATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGC 523 	404 TCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATA 463 	344 TCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTT 403 	284 GTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAAGCATGACCAGCAGT 343 	224 GAGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCCACACCTTTCG 283 [165 -GCGGCGTGCGGGCTGCACTGATTTGTGTGAGGGCCGCCGCGCGCG	105 GAGGCAGGCAGGCGGGCGGGGATGGTGTGCGCGGACTGCGGACTCCGCCGTTCCTCGC 164	GGCTCGCAAGGGAGCATCCCGAGCGGGCTCCGGGACGGCCGG 10 	Query Match 31.7%; Score 1610; DB 9; Length 2131; Best Local Similarity 85.5%; Pred. No. 0; Matches 1832; Conservative 0; Mismatches 295; Indels 15; Gaps 3;	/dev_stage="embryo, 10 weeks" /note="cloning vector: pME18SFL3" 694 a 469 c 526 g 442 t	<pre>/db_xref="taxon:9606" /clone="HEMBA1004110" /tissue_type="whole embryo, mainly head" /clone Tib="HEMBA1"</pre>		Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).	(E-mail:genomics@nri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction:	Direct Submission Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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7 GAGGAGGAGTGGAGCGCGGGAGGGCGCGCAGCTTGGTTGCTTCCGTAGTACGCCGCCT 66	/ Match 27.6%; Score 1404.2; DB 6; Length 2131; Local Similarity 81.0%; Pred. No. 1.2e-311; les 1740; Conservative 0; Mismatches 283; Indels 126; Gaps 4;	/mol type="genomic DNA" /db_xref="taxon:9606" 691 a 448 c 572 g 420 t	FT CDS	- 72	PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI PC C12N15/09.C07K14/47.C07K16/18.C12N1/15.C12N1/19.C12N1/21.C12N5/ PC	PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU PI SAITO.	OS Homo sapiens (human) PN JP 2002191363-A/13413		1 (bases 1 to 2131) Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Sai	Hon Eul	N Primer for synthesizing full-length cDNA and use thereof. BD158570 BD158570.1 GI:27864328 TP 2002191363-A/14413	BD158570	2141 GACTGAAGCAGAAAGAGCAGGAGAGAGAGAGCCTGGAGTTAG 2182	2081 AACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCAGCGC 2140	2021 TGGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGG 2080	1961 AAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGAGG 2020	1901 GTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCA 1960 	1841 AGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCA 1900 	1730 AAATTGAGAGCACAAACAAATCTAGAGAGTTGAGAATTGCCGAAATCACCCCATCTACAGC 1789
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Direct Submission

Direct Submission

Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

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NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology; cDNA library construction,

5'- & 3'-end one pass sequencing and clone selection: Helix

Research Institute (supported by Japan Rey Technology Center etc.)

Research Institute (supported by Japan Rey Technology Center etc.)
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University of Tokyo.
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JOURNAL
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REFERENCE
AUTHORS
TITLE REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 14 HSU61166 LOCUS DEFINITION TITLE Human SH3 U61166 U61166.1 1SU61166

GI:1438932

domain-containing protein

3241 bp

mRNA SH3P17

linear / mRNA, c

r PRI 23-JUL-1996 complete cds.

FEATURES JOURNAL M Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Mammalia; Eutheria; Primates; Catarrhini; Hominida;
1 (bases 1 to 3241)
Sparks, A.B., Hoffman, N.G., McConnell, S.J., Fowlkes
Sparks, A.B., defiman, N.G., McConnell, S.J., Fowlkes
Kay, B.K.
Cloning of ligand targets: systematic isolation of
domain-containing proteins
Jacoba (1996)
10224438 9630982 2 (base 2 (bases 1 to 3241)
Pirozzi.G., McConnell,S.J.,
Direct Submission
Submitted (18-UUN-1996) CYTO
Princeton, NJ 08540, USA Homo sapiens (human) Location/Qualifiers
1. .3241 /organism="Homo sapiens"
/mol_type="mRNA" CYTOGEN Uveges, A. and Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Corp., 307 Fowlkes, D Fowlkes, D.M. College Road 윥 East

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/tissue_type="bone marrow"
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AAAGAATGTATAGAAGTCTCCCTGAAATAAATTTCCCAAAGTTAAAAATTTTTTTAAATA
                                                                                        TTTTATTCCAGTTACTTTTCATGGAATGACCTATTTTGAACAAGTAATTTTCTTGACAAG
                                                                                                                        -TTTATTCCAGTTGCTTTTTATGGAA-----TATCTTGAACAAGTAATCTTCTTGACAAG
                                                                                                                                                                                     CACTGAGGTCGTTACGATCAACGATATCCACAGTCTCTTTTTAGTCTCTGTTACATGAAG
                                                                                                                                                                                                                                    TGCCCAGGCGGTTACGATCATCAGTACCCACCGTC----TTAGTCTCTGTTACGTGAAG
                                                                                                                                                                                                                                                                                                             GTTTTGTTTTATTTTCAATCTGGCATGTCTTCACACCATAAACTAGTAAGACGCCCAAC
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
JP 2002017375-A/3071
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PD 707-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KU
PI ISHII,
PI YURI KAWAI, AI WAKAWATSU, TOMOYASU SUGIYAWA,)
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PI TETSUJI OTSUKI,HISASHI KOGA
PC
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1 (bases 1 to 1676)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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ACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGC 305
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                                   TTTGTCCCTGGGGCGGCAGCGCGGACCCGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA
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Conservative
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mer for synthesizing full-length cDNA and use thereof PH K
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07-JUL-2000 JP 2000253172
TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Search completed: December 4, 2003, 21:34:01 Job time : 12044.2 secs

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Result
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-477-389-4
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Sequence 38, Appl Sequence 194, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 133, Appli Sequence 134, Appli Sequence 134, Appli Sequence 134, Appli Sequence 41, Appli Sequence 41, Appli Sequence 4, Appli
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; MOLECULE TYPE: US-08-630-915A-38

peptide

Query Match 32.8%; Score 2058.5; DB 4; Length 462; Best Local Similarity 79.3%; Pred. No. 4.8e-138; Matches 391; Conservative 13; Mismatches 18; Indels 71;

71;

Gaps

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RESULT 1 US-08-30.915A-38 Sequence 38, Application US/08630915A Patent No. 6309820 APELICANT: HOPEMAN, No. 6309820h APPLICANT: HOPEMAN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME NUMBER OF SEQUENCES: 277 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York CITY: New York COMPTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER: READABLE FORM: APPLICATION AUMBER: US/08/G30,915A FILING DATE: 03-APR-1996 CURRENT APPLICATION E36 ATTORNEY/GGNT INVERSE: US/08/630,915A FILING DATE: 03-APR-1996 ATTORNEY/GGNT NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 1101-174 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9909 TELEPHONE: AGA amino acids TYPE: anino acids TYPE: anino acids TYPE: anino acids TYPE: mino acids	ALIGNMENTS	28. 297 4.7 2101 1 US-08-467-781-4 Sequence 4, Appli 30 297 4.7 2101 2 US-08-483-924-4 Sequence 4, Appli 30 297 4.7 2101 3 US-09-452-294-1 Sequence 136, Appli 32 296 4.7 2101 5 VS-09-195-487-4 Sequence 136, Appli 32 296 4.7 2101 5 PCT-US93-06160-4 Sequence 4, Appli 33 296 4.7 2101 5 PCT-US93-06160-4 Sequence 2, Appli 35 281 4.5 1805 1 US-07-853-913-2 Pattent NO. 5210183 36 281 4.5 1805 1 US-07-853-913-2 Pattent NO. 5210183 37 280.5 4.5 1375 4 US-09-721-199-2 Sequence 2, Appli 38 280.5 4.5 1375 4 US-09-721-199-2 Sequence 2, Appli 40 275 4.4 1360 4 US-09-33-559-2 Sequence 2, Appli 42 275 4.4 1360 4 US-09-45-456A-34 Sequence 34, Appl 44 275 4.4 1360 4 US-09-45-324A-34 Sequence 34, Appl 45 274.5 4.4 1360 4 US-09-645-791-34 Sequence 34, Appl 45 274.5 4.4 1354 3 US-08-685-871-2
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US-08-630-915A-194
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APPLICANT: SPARKS,
APPLICANT: HOFFMAN
APPLICANT: KAY, B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 194, Application US/08630915A
Patent No. 6309820
                                                                                                                                                                                                                                                                                                                    APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,915A FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                         STREET: 1155 AV
CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
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US-08-630-915A-40

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Sequence 40, Application US/08630915A Patent No. 6309820

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: HOFFMAN, No. 6309820h

APPLICANT: KAY, Brian K.

APPLICANT: FOWLKES, Dana M.

APPLICANT: MCCONNELL, Stephen J.

APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

TITLE OF INVENTION: USING SAME

ADDRESSEE: I NUMBER OF SEQUENCES:

ADDRESS:

& Edmonds LLP

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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
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TOPOLOGY: un
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LSFSKGQLINVMNKDDPDWWQGEINGVTGLFPSNYVKMTTDSDPSQQ 509
                  LAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                    GELQARGKKRQKGWFPASHVKLLGPSSERATPAFHP------VCQVIAMYDYAANNEDE
                                                                                                     GELOARGKKROIGWFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDE 1166
                                                                                                                                                              YVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWE 1100
                                                                                                                                                                                                            KKPTSAAYSVGEEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSN
                                                                                                                                                                                                                                                                                  KHDIITVLEQQENWWFGEVHGGRGWFPKSYVKIIPGSEVK-----REEPEALYAAVN
                                                                                                                                                                                                                                                                                                    KSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGFTESPASLKRVAS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAA
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                                                                                                                                        YVKPKDQESFGSASKSGASNKKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQ
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(212) 869-8864/9741
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; Pred. No. 1.9e-90;
85; Mismatches 124;
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                                                                                                                                                                                                                                    Sequence 2, Application US/08095737 Patent No. 5487979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                         GENERAL INFORMATION:
APPLICANT: Difiore, Pier P
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
TITLE OF INVENTION: Factor Receptor Kinase
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                      CORRESPONDENCE ADDRESS:
STATE: Cali
COUNTRY: Un
ZIP: 92660
                          ADDRESSEE: Knobbe, Martens, Olson
STREET: 620 Newport Center Drive,
CITY: Newport Beach
STATE: California
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                                                                                                                                                                                                                                                                                                                                               GVTGLEPSNYVKMTTDSDPSQQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                     SSERATPAFHP-----VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWWQGEIN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHVKLLGP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASNKKPEI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 816.5; DB 4; ilarity 58.4%; Pred. No. 2.6e-50; Conservative 38; Mismatches 54;
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                 States of America
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Sixteenth
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Best Local Similarity
Matches 198; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/095,737
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642
                                    511 WCSSPHSILVNGATDYCSLSTSSSETANLNEHVEGQSNLESEPIHQESPARSSPELLPSG
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                                                                                                                                                                                                 QLKEVRKKCAEBAQLISSLK-----
                                                                                                                                                                                                                                      KLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQ
                                                                                                                                                                                                                                                                                NTNLQKLQAQKQ-----QVQELLDE-----------LDEQKAQLEE
                                                                                                                                                                                                                                                                                                                                                                 LQREK-----NNVEQDLKEKE------DTIKQRTSEVQ---DLQDEVQRE
                                                                                                                                                                                                                                                                                                                                                                                                      QQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQRELERQREEERRKEIERR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLQKNIIGSSPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAM-SGQPLPPVLPPEYIPPSFRRVRS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KT------WVVSPAEKAKYDEIFLKTDKDMDGFVSGLEVREIFLKTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVEFSIAMKLIKLKLQGYQLESTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPVPM 134
                                                                                                                LQQETAE-----LEESVESGKAQLEPLQQHLQDSQQEISSMQMKLMEMKDLENHNSQLN
                                                                                                                                                       VQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRS-----KLQEIDVFNNQLK 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSTLLAHIWSLCDTKDCGKLSKDQFALAFHLISQKLIKGIDPPHVLTPEMIPPS---DRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL 194
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257 254

Qy 15 WAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMD	Query Match 7.8%; Score 486.5; DB 1; Length 896; Best Local Similarity 20.5%; Pred. No. 4.3e-26; Matches 198; Conservative 150; Mismatches 273; Indels 345; Gaps	amino acid Y: linear TYPE: prote	; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS; ; LENGTH: 896 amino acids	; TELEPHONE: (619) 235-8550 ; TELEFAX: (619) 235-0176	REGISTRATION NUMBER: 02,655 REFERENCE/DOCKET NUMBER: NIH060.001A FELECOMMINICATION INFORMATION	110	; APPLICATION NUMBER: 05/08/480,145 ; EILING DATE: 07-JUN-1995 ; CLASSIFICATION: 530 ; PRIOR APPLICATION DATA:	ARC	; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; CDEBATING CYCTEM TO TOCK TOCK	; COUNTRY: United States of America; ZIP: 92660; COMPUTER READABLE FORM:	E: Knobbe, Mart 620 Newport Cer ewport Beach California	ボロママ	; GENERAL INFORMATION: ; GENERAL INFORMATION: ; APPLICANT: DiFlore, Pier P ; APPLICANT: Fazioli, Francesca	RESULT 5 US-08-480-145-2 ; Sequence 2, Application US/08480145 · Parent No. 5717067	Db 846 FSAYPS 851	Qy 866 WAAQPS 871	QY 831VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDT	Db 735 NEDPFRSATSSSVSNVVITKNVFEETSVKSEDEPPALPPKIGTPTRPCPLP	Qy 781ELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP	QY 739 KVVYXRALXPFESRSHDEITIQPGDIVMVDESQTGEPGWLGG	623 DPFVGSDPFKDDPFGKIDPFGGDPFKGSDPFASDCFFRQSTDPFATSSTDPFSAANNSSI	QY 695AKPEMODKQSRLFHEHQEPAKLATQAPWSTTEKGPLTISAQESV	Db 571 VTDENEVTTAVTEKVCSELDNNRHSKEEDPFNVDSSSLTGPVADTNLDFFQS
74 ; GENERAL INFORMATION:	RESULT 6 US-08-477-389-2 US-08-477-389-2 ; Sequence 2, Application US/08477389 . Parent No 2, R37219	Qy 866 WAAQPS 871 :: Db 846 FSAYPS 851	Db 786 PGKRSINKLDSPDFFKLNDFFQPFFGNDSPKEKDPEMFCDPFTSATTTTNKEADPSNFAN 845	831VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDT	Qy 781ELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP 830	Qy 739 KVVYYRALYPPESRSHDEITIQPGDIVMVDESQTGEPGWLGG 780	FSAANNSSI	571 VTDENEVTTAVTEKVCSELDNNRHSKEEDPFNVDSSSLTGPVADTNLDFFQS	Qy 642 EKOKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER 694	Qy 608 ELREHIS	554 VQNSLHROSLITIKRALEAKELARQQIREQLISEVERTRSKLQBIDVFNNQIK	Qy 494 KLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQ 553 : :	Db 381 NTNLQKLQAQKQQVQELLDELDEQKAQLEE 410	Db 345 LQREKNNVEQDIKEKEDTIKQRTSEVQDLQDEVQRE 380	315	Qy 314 GSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLE 373	865 Qy 255 PQAQLASIWRLSDIDQDGKLTAEEFILAMHLIDVAM-SGQPLPPVLPPEYIPPSFRRVRS 313	785 Db 216 KTWVVSPAEKAKYDEIFLKTDKDMDGFVSGLEVRBIFLKTGL 257	830 QY 195 NTKLQKAQSEDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL 254	780 QY 135 GSIEVVGMSPPLVSVPPAAVPPLANGAPPVIQPLPAFAHPAAIWPKSSSFSKSGEGSQL 194 : : 734	Db 182	738 QY 75 QVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPVPM 134	622 Db 122 WAVKPEDKAKYDAIFDSLSFVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLD 181

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NAME: IBraelsen, Neu A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TOTOPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 235-017
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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LQREK------NNVEQDLKEKE--
                                                                                     QQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQRELERQREEERRKEIERR 433
                                                                                                                             SLQKNIIGSSPV--
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                                                                                                                                                                                                                                                                                                         NTKLOKAOSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL 254
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                                                                                                                                                                                                                                   PQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAM-SGQPLPPVLPPEYIPPSFRRVRS 313
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620 Newport Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 486.5; DB 2;
20.5%; Pred. No. 4.3e-26;
ative 150; Mismatches 273;
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
                          NAME: Israelsen, Ned A REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-850
                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: 19930722
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Drive,
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Sixteenth Floor
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 897 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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843 WADFSST-----WPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGSS 895
                                                           740 AFNPTISSSTSSVTIAKPMLEETASKSEDVPPALPPKVGTPTRPCPPP-----PGKRPIN 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 QLQEVRKKCAEEAQLISSLK-----ABITSQESQISSYEEELLK-----AREELSR 456
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                                                                                                                                                                                                                                                                             703
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                                                                                                                                                 SSNTSVETWKHNDPFAPGGTVVAAASDSATDPFASVFGNESFG-DGFADFSTLSKVNNED 739
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                                                                                                     VPTP-----AKPVTDLTSA-----PA--PKLALRETPAPLPVTSSEPSTTPNN 842
                                                                                                                                                                                                                                                                           KT------WVVSPAEKAKYDEIFLKTDKDMDGYVSGLEVRETFLKTGL 257
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896 PSP 898 896 ADD 841 896 AND 841 897 ADD 841 898 ADD 841 898 ADD 841 898 ADD 841 898 ADD 841 899 AD																							***													
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RESULT 9
US-08-477-389-4
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                                                                                                                                   APPLICANT: DiFiore, Fig. APPLICANT: DiFiore, Francesca
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Gro
TITLE OF INVENTION: Factor Receptor Kinase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                     COUNTRY:
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                                                                                                                         United States of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 897 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: ISTAELSEN, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-JUL-1993
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                                                                                                                                                                                                                                       411 QLQEVRKKCAEEAQLISSLK-----AEITSQESQISSYEEELLK-----AREELSR
                                                                                                                                                                                                                                                                           494 KLODIRCRLATOROEIESTNKSRELRIAEITHLOOOLOESQOMLGRLIPEKQILSDOLKO
                                                                                                                                                                                                                                                                                                                  381 SINLOKLOAOKO-----OVOELLGE
                                                                                                                                                                                                                                                                                                                                                                                             345 LQREK-----NNVEQDLKEKE-------DTVKQRTSEVQ---DLQDEVQRE
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      PETAPSDVTDESEAVTVAGNEKVTPR--FDDDKHSKEEDPFNVESSSLTDAVADTNLDFF
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                                        ER------DKOWLEHVOOEEOPRPRKPHEEDRLKREDSVRKKEA----EERAKPEMODK 702
                                                                                                                     LREIHSKQQLQKQ-----
                                                                                                                                                            LQQETAQ-----LEESVESGKAQLEPLQQHLQESQQEISSMQMRLEMKDLETDNNQ---
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                                                                                 SNWSSSPQSVLVNGATDYCSLSTSSSETANFNEHAEGQNNLESEPTHQESSVRSS
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                                                                                                                     ----RSLEAARLKQKEQERKSLELEKQKEDAQRRVQ
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US-08-728-323A-2
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                                                                                             ; MOLECULE TYPE:
US-08-728-323A-2
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GENERAL INFORMATION:
                                                                                                                    TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                           Matches
                                                                 Query Match
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APPLICANT:
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                        TELEPHONE: 212-2.0525
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                      Local
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327 QRLPE--EPSSEDEQQ--PEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERL
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127; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1185 Avenue
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                                       6.1%; Score 382; DB 2;
larity 24.6%; Pred. No. 1.6e-18;
Conservative 139; Mismatches 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bohenzky, Roy A. Russo, James J.
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                                                                                                         protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunham LLP
of the Americas
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                                                                 Length 1162;
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                                         54;
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RESULT 11
US-09-298-568-2
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                      Sequence 2, Applion Patent No. 6322791
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Mary E.
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; ORGANISM: Kaposi's US-09-298-568-2
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                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                        LENGTH: 1162
TYPE: PRT
                                      383 AQLERAEQERKERERQEQEAKROLELEKOLEKORELEROREEERRKEIERREAAKRELER 442
                                                                                                                                                                127;
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QRLPE--EPSSEDEQQ--PEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERL 382
                                                                               Conservative
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                                                                                                                                                                                   6.1%;
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Pred. No. 1.6e-18;
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US-09-410-399-2
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LENGTH: 1162
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APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT FAPLICATION NUMBER: US/09/410,399
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                                                                           Matches 136;
                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (714) 760-950
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth
CITY: Newport Beach
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Pred. No. 3.9e-18;
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RESULT 14
US-08-800-644-94
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                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                          REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3
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                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0:
FILING DATE: 14-FEB-1997
CLASSIFICATION: 424
                                    TOPOLOGY:
                                                                                                                                                                                               NAME: Fedrick, Michael REGISTRATION NUMBER: 30
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US-08-475-894-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Yen-Mi
                                             FILING DATE:
CLASSIFICATION: 530
ATTORNEY_AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE_DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yen-Ming
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
              TELEPHONE:
                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
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              : (617)227-7400
(617)227-5941
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Pred. No. 3.9e-18
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-475-894-2
Search completed: December 4, 2003, 15:21:35 Job time: 28 secs
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                                                                               1109 LQARGKKRQIG-WFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDEL 1167
                                                                                                                                                                                                                                                                                                1055 GSGTAGKTGSLGKKPEIAQVIASYAATGPEQL-----TLAPGQLILIRKKNPGGWWEGE 1108
                                                                                                                                                                                                                                                       252 GSESDGGDSS-STKSEGANGTVATAAIQPKKVKGVGFGDIFKDKPIKLRPRS----IEVE 306
                                                                                                                                                                       307 NDFLPVEKTIGKKLPAT---TATPDSSK---TEMDSRTKSKDYCKVI--FPYEAQNDDEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                   137 LTNKAP-EKP--LHEV--PSGNSLLSSETTLRTNKRGERRRRRCQVAFSYLPQNDDELEL 191
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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              2058.5
1338.5
1330.5
816.5
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431.5
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6269
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/ Cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_N
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/cgn2_6/ptodata/1/pubpaa/USG6_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USG8_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USG8_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USG8_PUBCOMB.pep:*
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509
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                         0 US-09-764-868-738
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US-09-864-761-34169
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US-09-879-957-194
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6635.241 Million cell updates/sec
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                       Sequence 38, Appl
Sequence 194, App
Sequence 738, App
Sequence 40, Appl
Sequence 25, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 33620, A
Sequence 33635, A
Sequence 45565, A
Sequence 45565, A
Sequence 34169, A
Sequence 34169, A
Sequence 34169, A
Sequence 34169, A
                                                                                                                                                                                                                             Description
Sequence 128,
Sequence 2, Ap
Sequence 83, 1
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-0, Application (19-0); Sequence 38, Application (19-0); Patent No. US20020034755A1; GENERAL INFORMATION; Applicant: Applicant: HOFPMAN, No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-879-957-38
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929	888	1133	1133	2383	1200	1135	57	1070	1233	1212	1175	1175	1175	611	611	811	56	62	1564	1564	1170	287	784	735	59	659	1239	779	843
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US-09-298-523B-60	US-09-893-519A-73	US-10-309-851-16	US-10-309-851-14	-10-082-830-	US-10-094-749-2682	US-10-309-851-12	US-09-879-957-136	US-10-128-714-8314	US-09-291-417-89	US-10-247-671-157	US-09-771-161A-226	US-09-771-161A-225	US-09-771-161A-224	US-10-321-856-81	US-09-216-393-81	US-10-128-714-3314	US-09-879-957-134	US-09-879-957-135	US-10-144-198-4	US-10-144-198-2	US-10-341-434-95	US-09-764-868-744	US-10-144-194A-108	US-10-144-194A-109	US-09-879-957-133	US-10-144-621-2	US-09-291-417-13	-10-144-	US-10-144-194A-84
60,	73,	Sequence 16, Appl	14,	Sequence 260, App	2682	æ	136		89	15	22	Sequence 225, App	22,	e 81	Sequence 81, Appl	Sequence 3314, Ap	Sequence 134, App	Sequence 135, App	Sequence 4, Appli	Sequence 2, Appli	Sequence 95, Appl	Sequence 744, App	Sequence 108, App	e 10	133		13	86	Sequence 84, Appl

ALIGNMENTS

APPLICANT: SPARKS, Andrew B.

KAY, Brian K.

FOWLKES, Dana M.

MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND METHODS OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND METHODS OF IDENTIFYING AND METHODS OF IDENTIFYING AND DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND STATES IN THE PROPERTY OF A POLYPER POLYPE PO

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TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-879-957-38
                                                                                                                                                                                                                                                                                      US-09-879-957-194
Sequence 194, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
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Best Local :
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Local Similarity 79.3%; Pred. No. 2.6e-101;
hes 391; Conservative 13; Mismatches 18;
                                                                                                                                        APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWIKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
DOMAIN OF INTEREST AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081
                                                              NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGSSSPSPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVKLTTDMDPSQQ 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSN 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVK 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNWADFSSTWPTSTNEKPETDNWDAWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVL
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                                          ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                         YVKLTTDMDPSQQ 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPKSTALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLFPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGEKVEGLQAQALYPWRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGQKGWFPKSYVK
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TELEFAX: (212) 869-8864/9741
                         New York
                                                                                                                            USING SAME
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                                                                                                                                             AND METHODS OF
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HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-879-957-194
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UNMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECHMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
                                                                                   1107
    1167 LAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                                                                                                   1047 YVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWE 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                            410
                                                                                                                            350
                                                                                                                                                                                                                                                                                                                                                                           181 FSNLTVNTSWQ--KKSAFTRTVSPG-SVSPIHGQGQVVENLKAQALCSWTAKKDNHLNFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      751 SRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIP--ENEVPTPAKP 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 EEERKAEEKQ------RETASV------LVNYRALYPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                        GBLQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDE 1166
                                                                                                                                                                                                             KKPTSAAYSVGEEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSN
                                                                                                                                                                                                                              --PAAKPAIPGEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSN 1046
                                                                                                                                                                                                                                                                                                                                                                                                                  QPSLIVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFN 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEERAKPEMODKOSRLEHPHOEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFE 750
                                          GELQARGKKRQKGWFPASHVKLLGPSSERATPAFHP-----VCQVIAMYDYAANNEDE
                                                                                                                                                                                                                                                                                            KHDIITVLEQQENWWFGEVHGGRGWFPKSYVKIIPGSEVK------REEPEALYAAVN
                                                                                                                                                                                                                                                                                                                                 KSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KAVSPKKAL-----LPPTVSLSATS-----TS9EPLSSNQPASVTDYQN-VS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 509 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                              YVKPKDQESFGSASKSGASNKKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQ 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARNHDEMS FNSGDI I QVDEKTVGE PGWLYGS FQGNFGWF PCNYVEKMPSSENE - - - - - - -
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Pred. No. 8.3e-66;
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RESULT 4
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US-09-764-868-738
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APPLICANT: ROSen et al.
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                    Sequence 40, Application UP Patent No. US20020034755A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 738, Application US/09764868 Patent No. US20020168711A1
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Best Local (
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TYPE: PRT
ORGANISM: Homo sapiens
-09-764-868-738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - refer to NUMBER OF SEQ ID NOS: 1510
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                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        891 ATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQ 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPAT
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                                                                                                                                                                                                       EVSGQVGLFPSNYVKLTTDMDPSQQ 1213
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                                                                                                                                                                                                                                                                                                                                                                                      VEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASNKK
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQGDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKK 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGWFPKSYVKIIPGSEVK-----REEPEALYAAVNKKPTSAAYSVGEEYIALYPYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPG-SVSPIHGOGOVVENLKAOALCSWTAKKDNHLNFSKHDIITVLEQQENWWFGEVHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTVSLSATS-----TSSEPLSSNOPASVTDYON-VSFSNLTVNTSWQ--KKSAFTRTV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEPGWLYGSFQGNFGWFPCNYVEKMPSSENE-----KAVSPKKAL-----LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEPGWLGGELKGKTGWFPANYAEKIP--ENEVPTPAKPVTDLTSAPAPKLALRETPAPLP 830
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                                                                                                       Application US/09879957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 1330.5; Dilarity 52.7%; Pred. No. 1e-62; Conservative 71; Mismatches 1
                      SPARKS, Andrew B. HOFFMAN, No. US20020034755Alh KAY, Brian K.
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RESULT 5
US-09-764-881-133
; Sequence 133, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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US-09-879-957-40
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Best Local S
Matches 153
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les 153; Conserv
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ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                        1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DDS/MS-DDS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                     1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                114
    227
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                     GQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                                                   GTSKITPTELPKTĄVQPAVCQVIGMYDYTAQNDDELAPSKGQIINVLNKEDPDWWKGEVS 1191
                                                                                                                                                                                                                                                                    GDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEI
                                                                                SSERATPAFHP----
                                                                                                                                                            AQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHVKLLGP
                                                                                                                                                                                          AQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSP
                                                                                                                                                                                                                                             GDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASNKKPEI
                                                                                                                                                                                                                                                                                                                             FAAASTKIIPGSEVK------REEPEALYAAVNKKPTSAAYSVGEEYIALYPYSSVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
GVTGLFPSNYVKMTTDSDPSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 248 amino acids
TYPE: amino acid
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STREET: 1155 Avenue of the Amer
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                - VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWWQGEIN
                                                                                                                                                                                                                                                                                                                                                                                                           38;
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Pred. No. 6.7e-36;
8; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 248;
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                                                                                                                                                                                                                                                                                                                                Sequence 25, Applica Patent No. US2002017 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed -
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 133
LENGTH: 144
TYPE: PRT
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows
SEQ ID NO 25
                                                                   Matches
                                                                               Query Match
Best Local
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Best Local
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                                                                                                                    LENGTH: 813
TYPE: PRT
ORGANISM: Homo Sapien
-09-964-899-25
                                                                                                                                                                                                                                                         APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in TITLE OF INVENTION: Alzheimer's Disease Using Drosophil FILE REFERENCE: 4-31612 A CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZO7
FILE REPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                        CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/298,309
PRIOR FILING DATE: 2001-06-14
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NAME/KEY: SITE
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LOCATION: (143)
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LOCATION: (134)
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                   105
                                                                  al Similarity
197; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLIKLKLQGYQLPSALPPVMKQQPVAISSAPALVWGGIASKPPLTAVAPVPMGXIPVVG
                   EDKAKYDAIFDSLSPVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLDRDEFA
                                         EERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMDQVEFS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KERHDQQFHSLKPISGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMDQVEFSIA
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                                                                                                                                                                                                                                                                                                                                                             Application US/09964899
                                                                 8.4%; Score 527; DB 10;
larity 21.9%; Pred. No. 5.6e-20;
Conservative 138; Mismatches 283
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                                                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 572; DB 11;
Pred. No. 3.1e-23;
6; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               refer to
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                                                                   283;
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                                                                                          Length 813;
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165 VAMPLVYCALEKEPVPMSLPPAL----VPPSKRKTVSISGSVRLIPSSASAKESYHSLPS 220
---PKIGTPTRPCPLPPGNDSPKEKDPEMFCDPFTSATTTTNKEADPSNFANFSAYPS
                                                        APAPKLALRETPAPLPVTSSEP-STTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPS 871
                                                                                                                           SFGGGFADFSTLSKVNNEDPFRSATSSSVSNVVITKNVFEETSVKSEDEPPALP-----
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                                                                                                                                                                                                                                                                                                                   STTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQT-----GEP
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RESULT 7

US-09-764-881-132
; Sequence 132, Application US/09764881
; Publication No. US20030125246A9
; Deblication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and i;
; FILE REFERENCE: PTZ07
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 132
; LENGTH: 224

Antibodies

file

wrapper

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US-09-864-761-33620
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OTHER INFORMATION: Xaa
-09-764-881-132
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (183)
OTHER INFORMATION:
NAME/KEY: SITE
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                   APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-08-03
                                  APPLICATION NUMBER: PCT/US01/00663
                                                     APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                          FILING DATE:
                                                                                                                                              APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: PCT/US01/0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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. US20020048763A1
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Chen, Wensheng
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Hanzel, David K.
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                 2001-01-30
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Pred. No. 1.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 224;
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FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PC7/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PC7/US01/00666
PRIOR APPLICATION NUMBER: PC7/US01/00667
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Patent No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
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o. US20020048763A1
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NN: EXPRESSED IN HELA, SIGNAL = 1.6

NN: EXPRESSED IN HEAIN, SIGNAL = 2.3

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6

NN: EXPRESSED IN BOTA MARROW, SIGNAL = 1.8

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

NN: EXPRESSED IN LUNG, SIGNAL = 1.6

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7

NN: EXPRESSED IN HEART, SIGNAL = 2.7
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Pred. No. 6.6e-16;
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00668
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SED IN BONE MARROW, SIGNAL = 1.3
SED IN HBL100, SIGNAL = 1.3
SSED IN FETAL LIVER, SIGNAL = 32
SSED IN LUNG, SIGNAL = 0.66
ESSED IN BRAIN, SIGNAL = 0.69
RESSED IN PLACENTA, SIGNAL = 0.1
RESSED IN PLACENTA, SIGNAL = 0.92
PRESSED IN ADULT LIVER, SIGNAL = 0.92
PRESSED IN ADULT LIVER, SIGNAL = 0.98
THUMAN HIT: AA773823.1, EVALUE 2.00e-45
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     GENERAL INFORMATION APPLICANT: Penn, SI
                                                     Sequence 46565, Application US/09864761
Patent No. US20020048763A1
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       Penn, Sharron G
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 33635
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APPLICATION NUMBER: PCT/US01/00667
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EXPRESSED IN HEALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN BONE MARROW, SIGNAL = 3.4
IN HELA, SIGNAL = 3.7
IN ADULT LIVER, SIGNAL = 3
IN LUNG, SIGNAL = 2.2
HIT: O35601, EVALUE 2.80e-01
HIT: AA815076.1, EVALUE 1.00e-08
                                                                                                                                                                                                                                                                                                              4.
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IN BT474, SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN FETAL LIVER, SIGNAL IN BRAIN, SIGNAL = 2.6
                                                                                                                                                                                                                                                                                                              Score 426; DB 9; 1
Pred. No. 1.1e-15;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEART, SIGNAL = 2.2
HBL100, SIGNAL = 3.
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Best Local
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PRIOR PILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: MAP TO
OTHER INFORMATION: EXPRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
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ENGTH: 82
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APPLICATION NUMBER: GB 24263.6
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00663
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827 APLPVTSSEPSTTPNNWADFSS 848
                                                                                                                                                   Similarity
                                                                VDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETP
                                        VDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETP
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                                                                                                                               Conservative
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N: EXPRESSED IN HELA, SIGNAL = 2.4

N: EXPRESSED IN PLACENTA, SIGNAL = 1.2

N: EXPRESSED IN PLATA, SIGNAL = 0.76

N: EXPRESSED IN HEL100, SIGNAL = 1.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95

N: EXPRESSED IN HOME WARROW, SIGNAL = 0.95

N: SWISSPROT HIT: Q15811, EVALUE 9.00e-45

N: EST_HUMAN HIT: AA773823.1, EVALUE 2.00e-37
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Pred. No. 1.4e
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1.4e-15;
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FILLE OF INVENTION: GRAP DEFENDED IN THE PETERENCE: ACONICA-X-1
CURRENT PETING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Annomax Sequence SEQ ID NO 34169
                                                          OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 87
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                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo
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APPLICATION NUMBER: PCT/US01/00661
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Chen, Wensheng
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Hanzel, David K.
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BED IN BOXE MARROW, SIGNAL = 3.3
BED IN ADULT LIVER, SIGNAL = 3.2
BED IN BRAIN, SIGNAL = 4
BED IN BRAIN, SIGNAL = 3.3
BED IN BT474, SIGNAL = 3.3
BED IN HBLIO, SIGNAL = 2.9
BED IN LUNG, SIGNAL = 3.2
BED IN LUNG, SIGNAL = 3.2
BED IN HELA, SIGNAL = 3.5
BED IN HELA, SIGNAL = 3.5
BED IN HELA, SIGNAL = 5.3
BED IN HEART, SIGNAL = 5.3
BED IN HEART, SIGNAL = 2.9
MAN HIT: AA815076.1, EVALUE 4.00e-09
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; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (165)
; OTHER INFORMATION: X
US-09-764-881-128
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US-09-764-881-128
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Matches
                                                                                                                                                        Query Match 6.5%;
Best Local Similarity 60.4%;
Matches 87; Conservative 1
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SEQ ID NO 128
SEQ II NO 128
TYPE: PRT
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 192
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
NAME/KEY: SITE
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NAME/KEY: SITE
LOCATION: (77)
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LOCATION: (147)
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OTHER INFORMATION:
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les 84; Conserv
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                                                                     IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG 118
                                                                                                                             MAQEPTPEGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFEFQSGLPQPVLAQ 60
                                                                                                      MAQFFTAMNGGPNMXAITSEERTKHDRQFDNLKPSGGYITGDQARNFXLQSGLPAFVLAE 67
                                                   IWALSDLNXXGKMDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGMG
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o. US20030125246A9
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Pred. No. 1.5e-14;
18; Mismatches 32
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Pred. No. 4.5e-15;
2; Mismatches 1
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RESULT 15 US-10-171-311-83

Sequence 83, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan

APPLICANT:

Chen, Yan Zhao, Xumei Monahan, John

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US-10-294-804-2
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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or
TITLE OF INVENTION: to Genomic Host DNA
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CURRENT APPLICATION NUMBER: US/10/294,804
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/410,399
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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                              ANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPA
                                                                SSSEDEMEVD-----YPVVS-THEQIASSPPGDNTPDDDPQPGPSREYRYVLRTSPPHRP
                                                                                             -SAQESVKVVYYRALYPFESRSHDEI-TIQPGDIVMVDESQTGEPGWLGGELKGKTGWFP 790
                                                                                                                                                              RIKREDSVRKKEAEERAKPEMQD----KQSRIFHPHQEPAKLATQAPWSTTEKGPLTI--
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Pred. No. 4e-12;
9; Mismatches 1
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
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Best Local Similarity
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SOFTWARE: FastSEQ for
SEQ ID NO 83
LENGTH: 2701
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APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DIDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
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                                      673 PRFQRQQEQMKQQQWQQQQQQQVLPQTVPSQPSSSTVPPPPHRPLYQPMQPHPQHLASMG
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                                                                                                                                                                                IRCRLATOROE----IESTNKSRELRIAEITH---------
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                                                                                                                                   QESENSCNKEEEPVFTRQDSNRS-EKEATPVVHETEPESGSQPRPAVLSGYFKQFQKSLP-672
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